Figure 1. Advantage of Efficacy-First Discovery™ Method
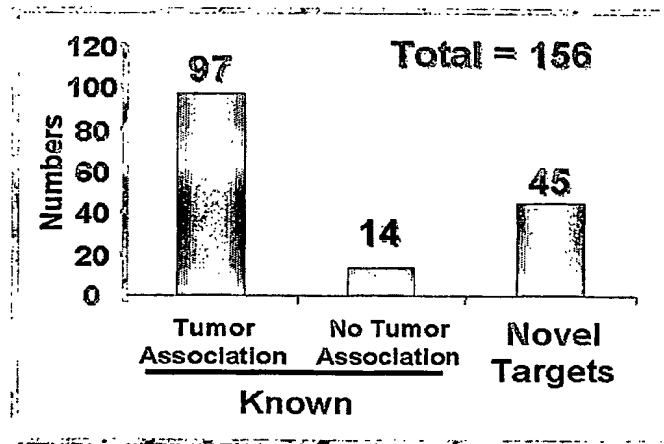
Figure 2. Highly Enriched Tumor Targets

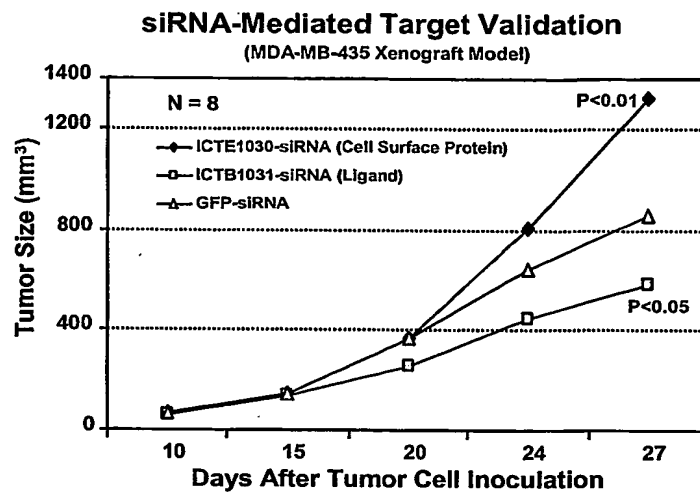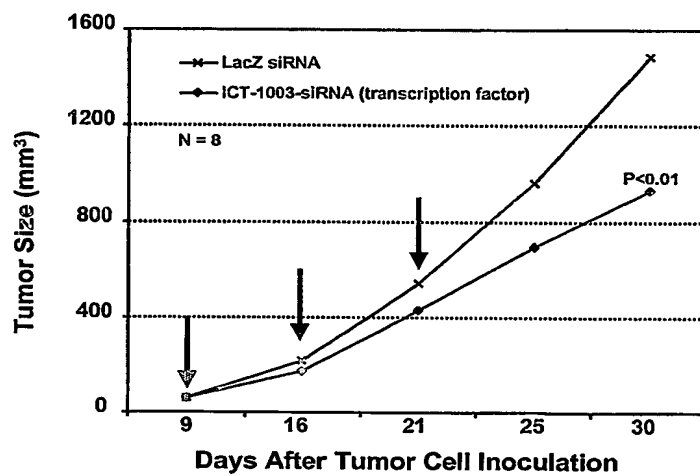## siRNA-Mediated Target Validation
(MDA-MB-435 Xenograft Model)

Figure 3. Two Novel Targets Were Validated

5

Figure 4. A Novel Targets Was Validated

10

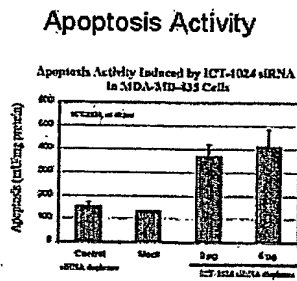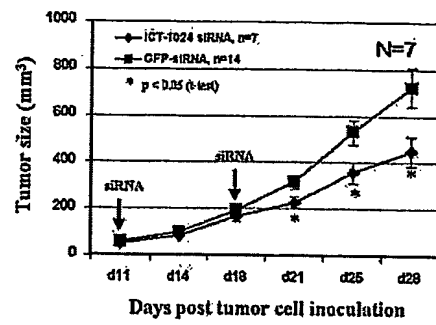**ICT1024,** <u>a growth factor receptor like protein</u>

In vivo
In vitro

Figure 5.

ICT1025, <u>a tumor reject antigen</u>

In vivo
In vitro

Apoptosis Activity
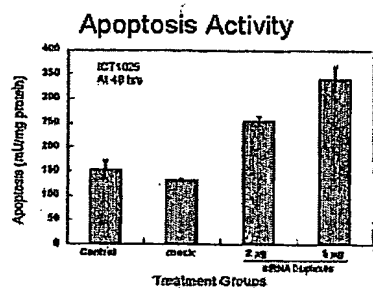
Xenograft tumor Inhibition
MDA-MB-435 cell induced tumor

Figure 6.

5
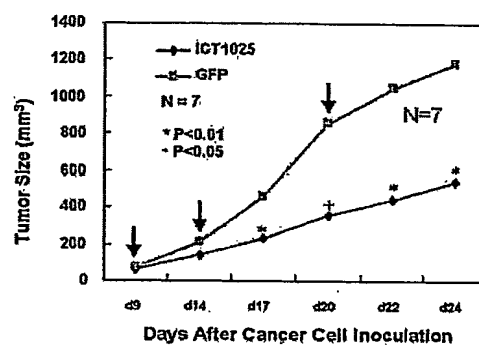
Figure 7

ICT-1024 siRNA Design:

ATG, 113   TGA 2678
                          ↓   ↓
hEGFR-RP ━━━
(mRNA, 2964 bp)
                     ↓   210 aagagcccagcttcctgcagc

                  ↓ 173 aagctggacattccctctgcg
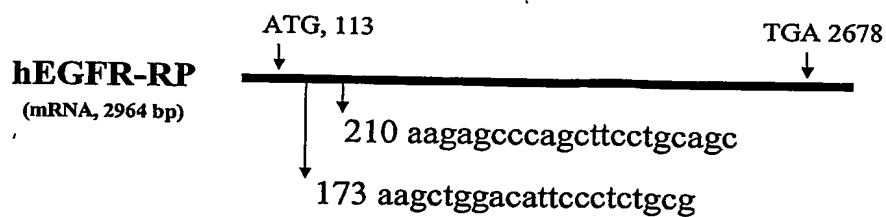
Figure 8.

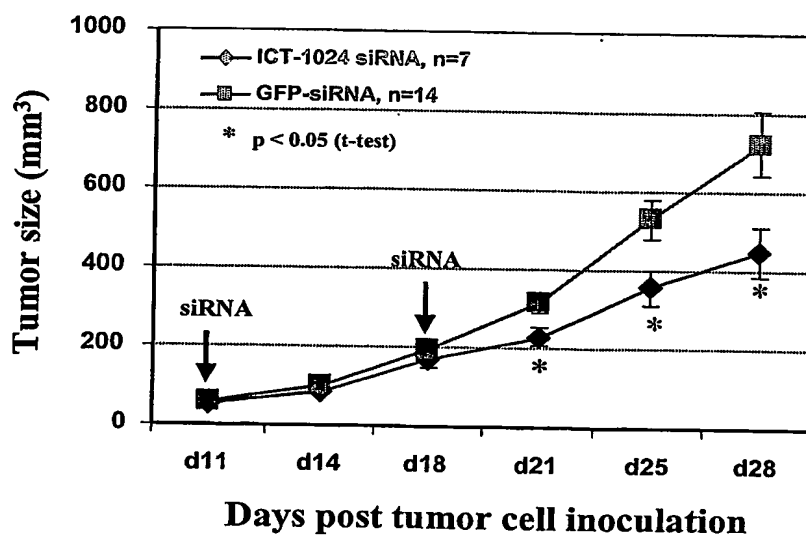## ICT-1024 siRNA mediated tumor growth inhibition in MDA-MB-435/nude mice model

Figure 9.

Apoptosis Activity Induced by ICT-1024 siRNA in MDA-MB-435 Cells

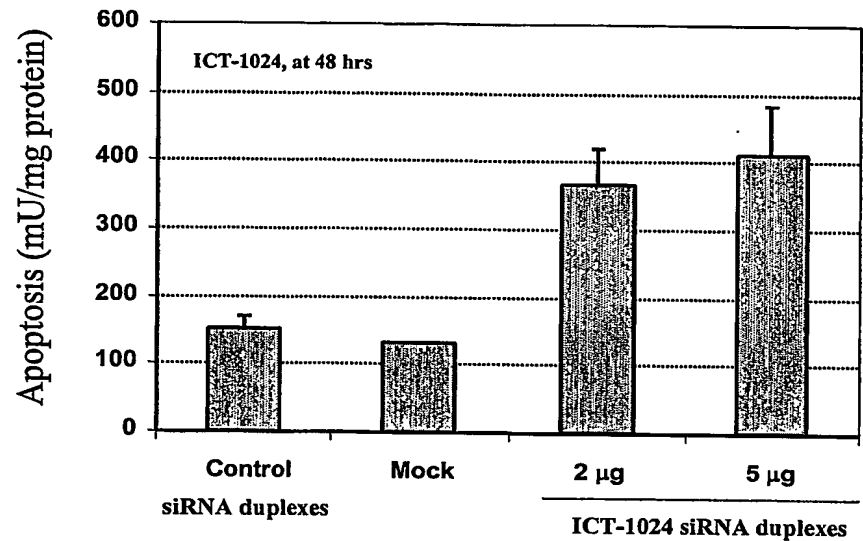Figure 10.   SAGE/Microarray Data

CGAP SAGE Expression Data and Correlation: ICT1024 has significantly positive correlation with other breast cancer genes
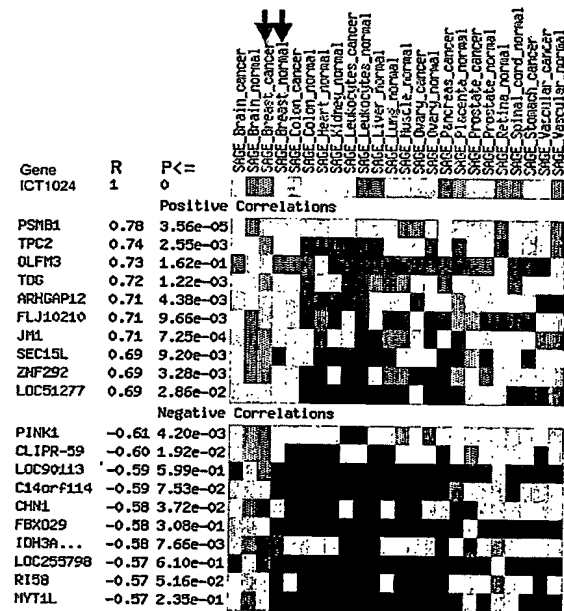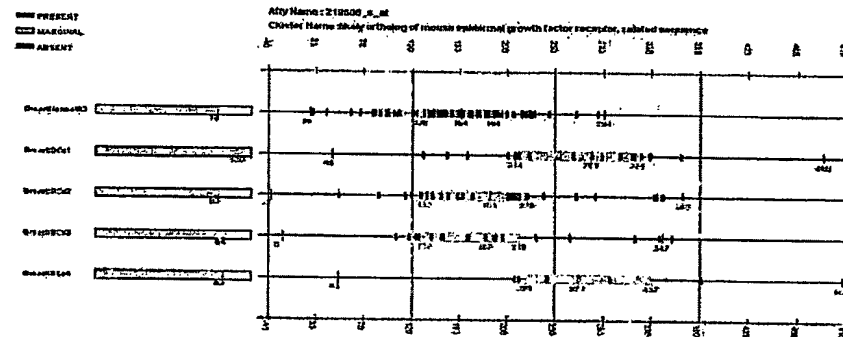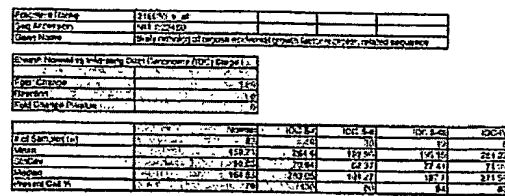
Figure 11　**Cancer Tissue Distribution**

ICT1024 is highly up regulated in all Stage I Breast Tumor samples (100%)

Figure 12.　Consensus in rhomboid family

```
                         10        20        30        40        50        60
                    ....*....|....*....|....*....|....*....|....*....|....*....|
Human    consensus    1  PLQPGQLWR--LITSMFLHAGILHLLFNMLSLLFFGIPLERRLGSVRFLLLYLLSGLAG-  57
Yeast    gi 9963865   99  ALRNMQVYR--LVTYIFVYENPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIPAIFS- 155
Bacteria gi 3738201   47  LLQKRQLYS--IITYVTLHLSMLHIVFNFVSLLPAMSQFEKKQGTLACILVTVIPYTLFp 104
Yeast    gi 1653749   49  PRSLEGLRG--IVFAPFLHADFGHLIANSVPFVVLAWLVMLQ-EVSDFWIVTIITMVVG- 104
Human    gi 13621505  60  sksnarpvvaigdaDIYSYRIWS-FFCQWINTIPCWSNRRRPLGLTPFLLLYVLSGVHG- 117
Bacteria gi 20139804 103  PEIGREEAWR--FISYMLVHAgVQHILGNLCMQLVLGIPLEMVHKGLRVGLVYLAGVIAG- 159
Human    gi 1169951  129  PTLKFEFWR--YFTHALMHPSLMHILFNLLWWHYLGGAVEKRLGSGKLIVIRSISALLS- 185
Bacteria gi 11066250 198  SNPASKVLCspMLLSTFSHPSLFHMAANMYVLWSFSSSIVNILGQEQFMAVYLSAGVIS- 256
Human    gi 13813618  68  yLVIKGYYSe-LFTSIFITNSFVDPIFNFISLYVIYLIFGSRAGKHEYGIPILAGILGN- 125
Plant    gi 9294149  242  IFKHKDLKR--LFLSAFYHVNEPHLVYNMiSLLWKGIKLETSMGSSEFASMVPTLIGMS- 298

                         70        80        90       100       110       120
                    ....*....|....*....|....*....|....*....|....*....|....*....|
Human    consensus   58  SLLSLLLSPAS-----TPSVGASGAIFGLLGALLVLLPLNRILLLNP--GAALFLLLGII 110
Yeast    gi 9963865  156  AIIFLSPEAVSs----LSKLGBVEDARGFTPVAFAMLGVTTVRSRMRraLVFGMVVPSVL 211
Bacteria gi 3738201 105  GIMHLIVYHFP1rkdyVSIAGLSGWAFAFISASCVHSPQRLISFFN-----LFSIPAYCF 159
Yeast    gi 1653749 105  GLGVWLIAPPN-----TVTVGASILIFGYLGPLLFRGWFQKNLASIV1-SIVVLVLYGSA 158
Human    gi 13621505 118  NAFTFWLTPETV------AAGASTSLFGLPAAIVVLSFLGKNQALKD1-GKSYQTLIV-V 169
Bacteria gi 20139804 160  SLASSIFDPLR------YLVGASGGVYALMGGYFMNVLVNFQEMIPA--FGIFRLLIIIL 211
Human    gi 1169951  186  GYVQQKFSGPW-------FGGLSGVVYALMGYVWLRGERDPQSG--------IYLQRGLI 230
Bacteria gi 11066250 257  NFVSYLGKVATgr--yGPSLGASGAIMTVLAAVCTKIPEGR-LA--------IIFLPMFTF 306
Bacteria gi 13813618 126  LLTVIFYSPFT------LSSGASGGIFGLLSYYTFYDFLKKDNLG----VYGLVFLVSVP 175
Plant    gi 9294149  299  QGVTLLLAKSL-----LLLFDYDRAYYNEYAVGFSGVLFAMKVVLNSq-AEDYSSVYGIL 352

                         130       140       150       160       170
                    ....*....|....*....|....*....|....*....|....*....|.
Human    consensus  111  LLMLLLGL---LPGISNFG-----------HLGGLLAGLLLGFLLLRRPR 146
Yeast    gi 9963865  212  VPWLLLGAsw1IPQTSFLS------------NVCGLSIGLAYAHLLLFHRP 250
Bacteria gi 3738201 160  PIIYLIMTti1VPKASFIG-----------HASGAVMGYCTPFMLGSIPL 198
Yeast    gi 1653749 159  LWGLLPGR----AGVSWQG------------HLFGFIGGAIAAWLIAREKH 193
Human    gi 13621505 170  NLLMNLF----MPNVSMAG-----------HIGGVVGGALLSIVFPTKMR 204
Bacteria gi 20139804 212  IIVLDMGF---ALYRRFFVpedgsp-vsfaaHIAGGPAGMSIGYTVPSCFD 258
Human    gi 1169951  231  IFALIWIV---AGWFDLFGmsma-----ngaHIAGLAVGLAMAFVDSLNAR 273
Bacteria gi 11066250 307  TAGNALKA---IIAMDTAGmilgwkffdhaaHLGGALFGIWYVTYGHELIW 354
Bacteria gi 13813618 176  GVSDLIPP-----NVNVVA------------HIGGILGGIMYAVVYYLIRS 209
Plant    gi 9294149  353  VPTKYAAWa-eLILVQMFVpnas-----flgHLGGILAGIIYLKLKGSYSG 397
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Figure 13.

Human rhomboid Proteins

Human Rhomboid Family Protein Alignments

Figure 14. **Function Domain Homology**

ICT-1024, A Novel Member of Rhomboid Family

- No significant homologies to neither DNA sequences nor protein sequences

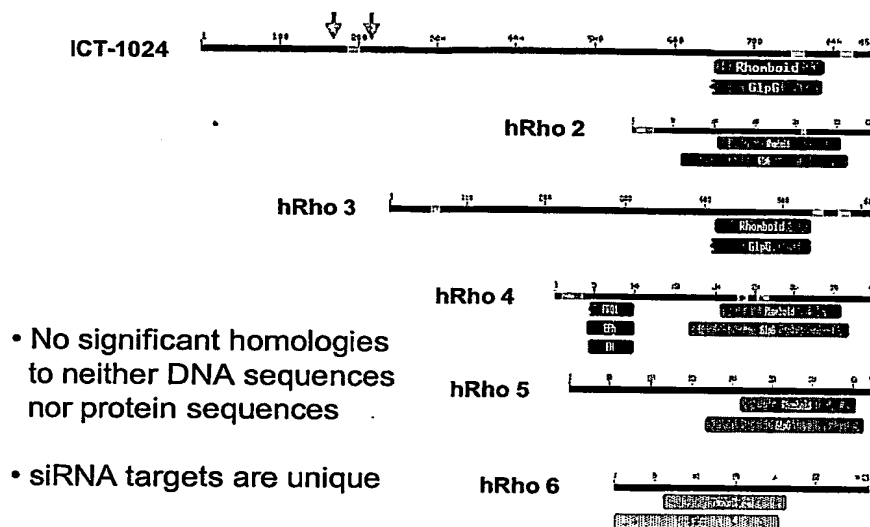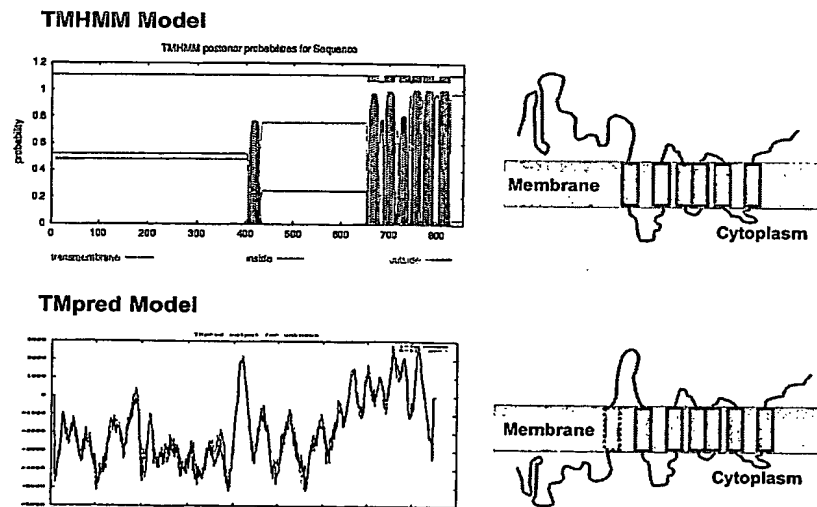- siRNA targets are unique

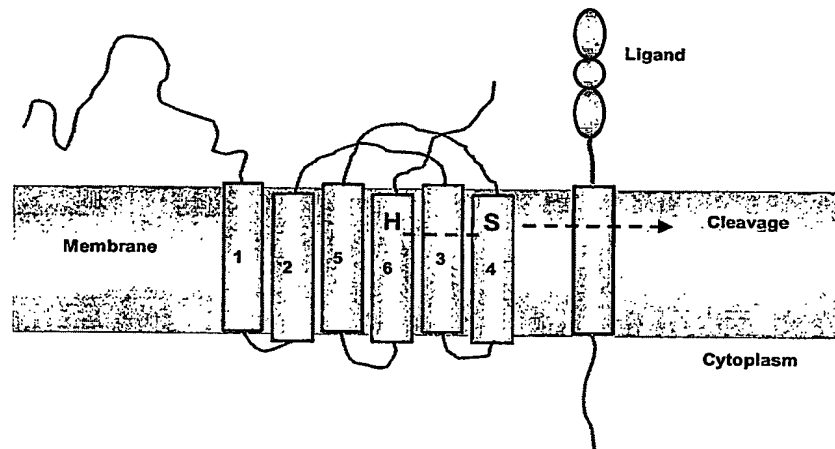Figure 15. **Hydrophobicity Analysis**

Cellular Location and Topology predictions

Activation of EGFRs and ligands

Figure 16.

ICT-1024 Intramembrane Protease Activity

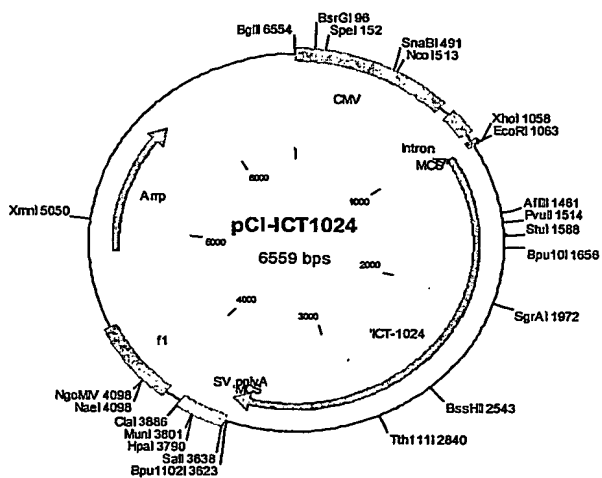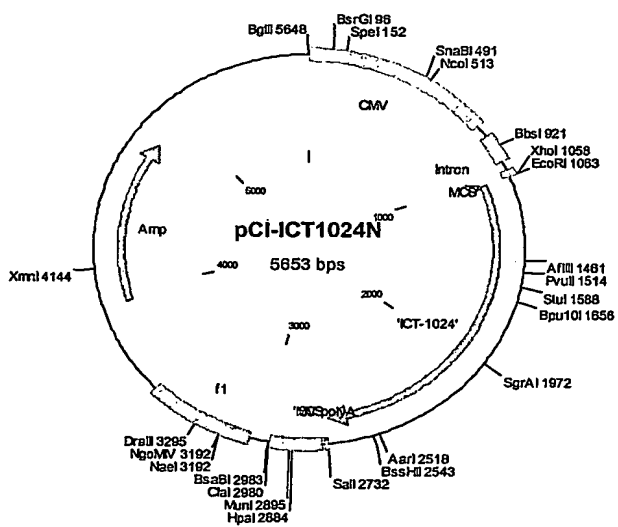*Refer to* **Koonin EV, et al.** *Genome Biology, 2003*

Figure 17.

Figure 18.

Figure 19.
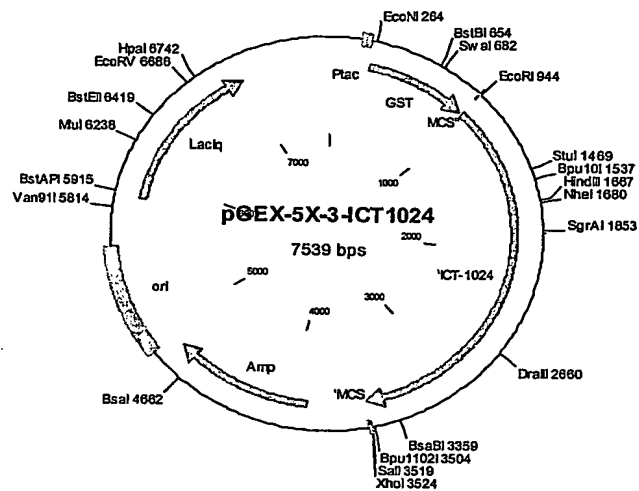
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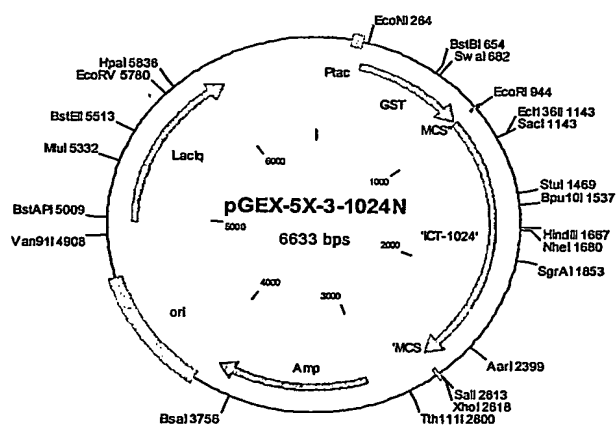
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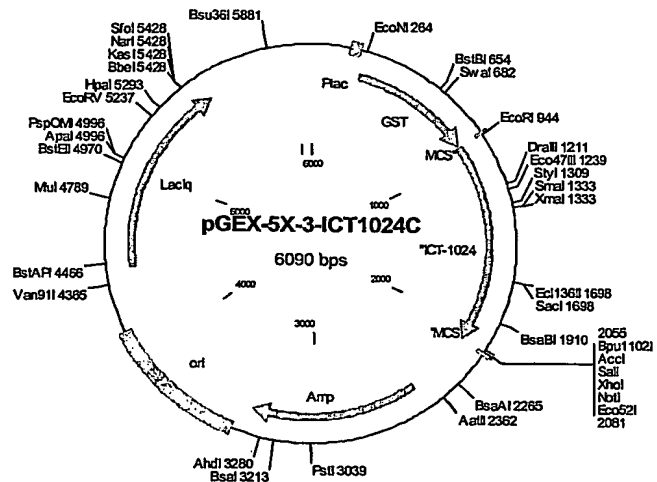
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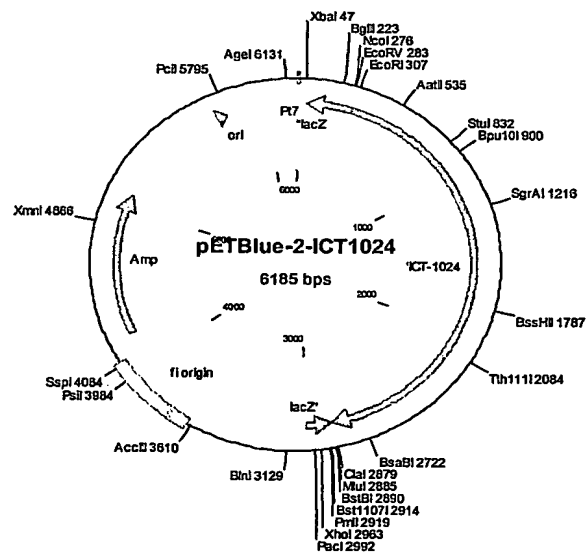
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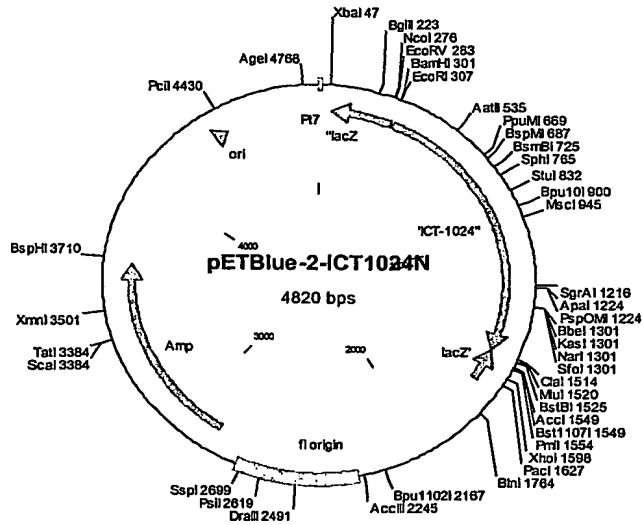
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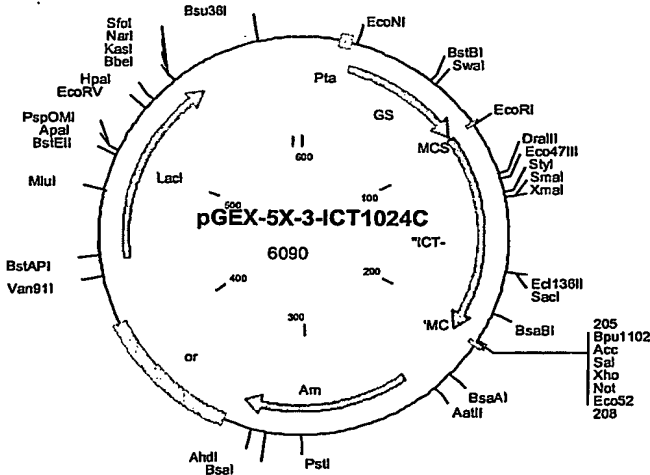
Fig. 25 (SEQ ID NO:58) ICT1024 PROTEIN (855 AA) CODING REGION: 1670-3637

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181   GTCATTAGTT  CATAGCCCAT  ATATGGAGTT  CCGCGTTACA  TAACTTACGG  TAAATGGCCC
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3061  CGGGATCTTG  CACTGCCTGG  TGTCCATCTG  CTTCCAGATG  ACTGTCCTGC  GGGACCTGGA
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5701   GGTGCCTCAC  TGATTAAGCA  TTGGTAACTG  TCAGACCAAG  TTTACTCATA  TATACTTTAG

5761   ATTGATTTAA  AACTTCATTT  TTAATTTAAA  AGGATCTAGG  TGAAGATCCT  TTTTGATAAT

5821   CTCATGACCA  AAATCCCTTA  ACGTGAGTTT  TCGTTCCACT  GAGCGGTCAGA CCCCGTAGAA

5881   AAGATCAAAG  GATCTTCTTG  AGATCCTTTT  TTTCTGCGCG  TAATCTGCTG  CTTGCAAACA

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Fig. 26 (SEQ ID NO:60) ICT1024 N TERMINUS 553 AA CODING REGION: 1070-2731

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241  GCCTGGCTGA CCGCCCAACG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT
301  AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC GGTAAACTGC
361  CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGTCCG CCCCCTATTG ACGTCAATGA
421  CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTACGGGACT TTCCTACTTG
481  GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAC
541  CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC CCATTGACGT
601  CAATGGGAGT TTGTTTTGGC ACCAAAAATCA ACGGGACTTT CCAAAATGTC GTAATAACCC
661  CGCCCCGTTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA TAAGCAGAGC
721  TCGTTTAGTG AACCGTCAGA TCACTAGAAG CTTTATTGCG GTAGTTTATC ACAGTTAAAT
781  TGCTAACGCA GTCAGTGCTT CTGACACAAC AGTCTCGAAC TTAAGCTGCA GAAGTTGGTC
841  GTGAGGCACT GGGCAGGTAA GTATCAAGGT TACAAGACAG GTTTAAGGAG ACCAATAGAA
901  ACTGGGCTTG TCGAGACAGA GAAGACTCTT GCGTTTCTGA TAGGCACCTA TTGGTCTTAC
961  TGACATCCAC TTTGCCTTTC TCTCCACACC CAGTTCAATT ACAGCTCTTA
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1021  AGGCTAGAGT ACTTAATACG ACTCACTATA GGCTAGCCTC GAGAATTCCA TGAGTGAGGC

1081  CCGCAGGGAC AGCACGAGCA GCCTGCGAGCG CAAGAAGCCA CCCTGGCTAA AGCTGGACAT

1141  TCCCTCTGCG GTGCCCCTGA CGGCAGAAGA GCCCAGCTTC CTGCAGCCCC TGAGGCGACA

1201  GGCTTTCCTG AGGAGTGTGA GTATGCCAGC CGAGACAGCC CACATCTCTT CACCCCACCA

1261  TGAGCTCCGG CGGCCGGTGC TGCAACGCCA GACGTCCATC ACACAGACCA TCCGCAGGGG

1321  GACCGCCGAC TGGTTTGGAG TGAGCAAGGA CAGTGACAGC ACCCAGAAAT GGCAGCGCAA

1381  GAGCATCCGT CACTGCAGCC AGCGCTACGG GAAGCTGAAG CCCCAGGTCC TCCGGGAGCT

1441  GGACCTGCCC AGCCAGGACA ACGTGTCGCT GACCAGCACC GAGACGCCAC CCCACTCTA

1501  CGTGGGGCCA TGCCAGCTGG GCATGCAGAA GATCATAGAC CCCCTGCCCC GTGGCCGTGC

1561  CTTCCGTGTG GCAGATGACA CTGCGGGAAGG CCTGAGTGCC CCACACACTC CCGTCACGCC

1621  GGGTGCTGCC TCCCTCTGCT CCTTCTCCAG CTCCCGCTCA GGTTTCCACC GGCTCCCGCG

1681  GCGGCGCAAG CGAGAGTCGG TGGCCAAGAT GAGCTTCCGG GCGGCCGCAG CGCTGATGAA

1741  AGGCCGCTCC GTTAGGGATG GCACCTTTCG CCGGGGCACGG CGTCGAAGCT TCACTCCAGC

1801  TAGCTTTCTG GAGGAGGACA CAACTGATTT CCCCGATGAG CTGGACACAT CCTTCTTTGC

1861  CCGGGAAGGT ATCCTCCATG AAGAGCTGTC CACATACCCG GATGAAGTTT TCGAGTCCCC

1921  ATCGGAGGCA GCGCTAAAGG ACTGGGAGAA GGCACCGGAG CAGGCGGACC TCACCGGCGG

1981  GGCCCTGGAC CGCAGCGAGC TTGAGCGCAG CCACCTGGG CTGCCCCTTGG AGCGAGGCTG

2041  GCGGAAGCAG AAGGAGGGCG CCGCAGCCCC CCGCAGCCCAAG GTGCGGCTCC GACAGGAGGT

2101  GGTGAGCACC GCGGGGCCGC GACGGGCCCA GCGTATCGCG GTGCCGGTGC GCAAGCTCTT
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2161   CGCCCGGGAG AAGCGGCCGT ATGGGCTGGG CATGGTGGGA CGGCTCACCA ACCGCACCTA
2221   CCGCAAGCGC ATCGACAGCT TCGTCAAGCG CCAGATCGAG GACATGGACG ACCACAGGCC
2281   CTTCTTCACC TACTGGCTTA CCTTCGTGCA CTCGCTCGTC ACCATCCTAG CCGTGTGCAT
2341   CTATGGCATC GCGCCCGTGG GCTTCTCGCA GCATGAGACG GTGGACTCGG TGCTGCGGAA
2401   CCGCGGGGTC TACGAGAACG TCAAGTACGT GCAGCAGGAG AACTTCTGGA TCGGGCCCAG
2461   CTCGGAGGCC CTCATCCACC TGGGCGCCAA GTTTTCGCCC TGCATGCGCC AGGACCCGCA
2521   GGTGCACAGC TTCATTCGCT CGGCGCGGCGA GCGCGAGAAG CACTCCGCCT GCTGCGTGCG
2581   CAACGACAGG TCGGGCTGCG TGCAGACCTC GGAGGAGGAG TGCTCGTCCA CGCTGGCAGT
2641   GTGGGTGAAG TGGCCCATCC ATCCCAGCGC CCCAGAGCTT GCGGGCCACA AGAGACAGTT
2701   TGGCTCTGTC TGCCACCAGG ATCCCAGGTG AGTCGACCCG GGCGGCGCGCT TCGAGCAGAC
2761   ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAACTA GAATGCAGTG AAAAAAATGC
2821   TTTATTTGTG AAATTTGTGA TGCTATTGCT TTATTTGTAA CCATTATAAG CTGCAATAAA
2881   CAAGTTAACA ACAACAATTG CATTCATTTT ATGTTTCAGG TTCAGGGGGA GATGTGGGAG
2941   GTTTTTTAAA GCAAGTAAAA CCTCTACAAA TGTGGTAAAA TCGATAAGGA TCCGGGGCTGG
3001   CGTAAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC
3061   GAATGGACGC GCCCTGTAGC GGCGCATTAA GCGCGGCGGG TGTGGTGGTT ACGCGCAGCG
3121   TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT CGCTTTCTTC CCTTCCTTTC
3181   TCGCCACGTT CGCCGGCTTT CCCCGTCAAG CTCTAAATCG GGGGCTCCCT TTAGGGTTCC
3241   GATTTAGAGC TTTACGGCAC CTCGACCGCA AAAAACTTGA TTTGGGTGAT GGTTCACGTA
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3301 GTGGGCCATC GCCCTGATAG ACGGTTTTTC GCCCTTTGAC GTTGGAGTCC ACGTTCTTTA

3361 ATAGTGGACT CTTGTTCCAA ACTGGAACAA CACTCAACCC TATCTCGGTC TATTCTTTTG

3421 ATTTATAAGG GATTTTGCCG ATTTCGGCCT ATTGGTTAAA AAATGAGCTG ATTTAACAAA

3481 TATTTAACGC GAATTTTAAC AAAATATTAA CGTTTACAAT TTCGCCTGAT GCGGTATTTT

3541 CTCCTTACGC ATCTGTGCGG TATTTCACAC CGCATATGGT GCACTCTCAG TACAATCTGC

3601 TCTGATGCCG CATAGTTAAG CCAGCCCCGA CACCCGCCAA CACCCGCTGA CGCGCCCTGA

3661 CGGGCTTGTC TGCTCCCGGC ATCCGCTTAC AGACAAGCTG TGACCGTCTC CGGGAGCTGC

3721 ATGTGTCAGA GGTTTTCACC GTCATCACCG AAACGCGCGA GACGAAAGGG CCTCGTGATA

3781 CGCCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT CTTAGACGTC AGGTGGCACT

3841 TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG

3901 TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT

3961 ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT

4021 GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA

4081 CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC

4141 GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC

4201 CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG

4261 GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA

4321 TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC

4381 GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT
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4441   GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG
4501   CCTGTAGCAA TGGCCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT
4561   TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC
4621   TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGGTCT
4681   CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT CCCGTATCGT AGTTATCTAC
4741   ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC
4801   TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT
4861   TTAAAACTTC ATTTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG
4921   ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAAGATC
4981   AAAGGATCTT CTTGAGATCC TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAAA
5041   CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG
5101   GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA
5161   GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTTA
5221   CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC AAGACGATAG
5281   TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG
5341   GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG
5401   CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG
5461   CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC
5521   CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG CCTATGGAAA
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5581  AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG

5641  GCTCGACAGA TCT
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Fig. 27, (SEQ ID NO: 61) ICT1024 coding region: 947-3518

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  1   TCGACTCGAG CGGCCGCCATC GTGACTGACT GACGATCTGC CTCGCGCGTT TCGGTGATGA

 61   CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTTGTC TGTAAGCGGA

121   TGCCGGGAGC AGACAAGCCC GTCAGGGCGC GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC

181   AGCCATGACC CAGTCACGTA GCGATAGCGG AGTGTATAAT TCTTGAAGAC GAAAGGGCCT

241   CGTGATACGC CTATTTTTAT AGGTTAATGT CATGATAATA ATGGTTTCTT AGACGTCAGG

301   TGGCACTTTT CGGGGAAATG TGCGCGGAAC CCCTATTTGT TTATTTTTCT AAATACATTC

361   AAATATGTAT CCGCTCATGA GACAATAACC CTGATAAATG CTTCAATAAT ATTGAAAAAG

421   GAAGAGTATG AGTATTCAAC ATTTCCGTGT CGCCCTTATT CCCTTTTTTG CGGCATTTTG

481   CCTTCCTGTT TTTGCTCACC CAGAAACGCT GGTGAAAGTA AAAGATGCTG AAGATCAGTT

541   GGGTGCACGA GTGGGTTACA TCGAACTGGA TCTCAACAGC GGTAAGATCC TTGAGAGTTT

601   TCGCCCCGAA GAACGTTTTC CAATGATGAG CACTTTTAAA GTTCTGCTAT GTGGCGCGGT

661   ATTATCCCGT GTTGACGCCG GGCAAGAGCA ACTCGGTCGC CGCATACACT ATTCTCAGAA

721   TGACTTGGTT GAGTACTCAC CAGTCACAGA AAAGCATCTT ACGGATGGCA TGACAGTAAG

781   AGAATTATGC AGTGCTGCCA TAACCATGAG TGATAACACT GCGGCCAACT TACTTCTGAC

841   AACGATCGGA GGACCGAAGG AGCTAACCGC TTTTTTGCAC AACATGGGGG ATCATGTAAC

901   TCGCCTTGAT CGTTGGGAAC CGGAGCTGAA TGAAGCCATA CCAAACGACG AGCGTGACAC

961   CACGATGCCT GCAGCAATGG CAACAACGTT GCGCAAACTA TTAACTGGCG AACTACTTAC
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1021  TCTAGCTTCC CGGCAACAAT TAATAGACTG GATGGAGGCG GATAAAGTTG CAGGACCACT

1081  TCTGCGCTCG GCCCTTCCGG CTGGCTGGTT TATTGCTGAT AAATCTGGAG CCGGTGAGCG

1141  TGGGTCTCGC GGTATCATTG CAGCACTGGG GCCAGATGGT AAGCCCTCCC GTATCGTAGT

1201  TATCTACACG ACGGGGAGTC AGGCAACTAT GGATGAACGA AATAGACAGA TCGCTGAGAT

1261  AGGTGCCTCA CTGATTAAGC ATTGGTAACT GTCAGACCAA GTTTACTCAT ATATACTTTA

1321  GATTGATTTA AAACTTCATT TTTAATTTAA AAGGATCTAG GTGAAGATCC TTTTTGATAA

1381  TCTCATGACC AAAATCCCTT AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA

1441  AAAGATCAAA GGATCTTCTT GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC

1501  AAAAAAACCA CCGCTACCAG CGGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT

1561  TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA GATACCAAAT ACTGTCCTTC TAGTGTAGCC

1621  GTAGTTAGGC CACCACTTCA AGAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT

1681  CCTGTTACCA GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT CTTACCGGGT TGGACTCAAG

1741  ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACACAGCC

1801  CAGCTTGGAG CGAACGACCT ACACCGAACT GAGATACCTA CAGCGTGAGC TATGAGAAAG

1861  CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC

1921  AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCGG

1981  GTTTCGCCAC CTCTGACTTG AGCGTCGATT TTTGTGATGC TCGTCAGGGG GGCGGAGCCT

2041  ATGGAAAAAC GCCAGCAACG CGGCCTTTTT ACGGTTCCTG GCCTTTTGCT GGCCTTTTGC

2101  TCACATGTTC TTTCCTGCGT TATCCCCTGA TTCTGTGGAT AACCGTATTA CCGCCTTTGA
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2161  GTGAGCTGAT ACCGCTCGCC GCAGCCGAAC GACCGAGCGC AGCGAGTCAG TGAGCGAGGA
2221  AGCGGAAGAG CGCCTGATGC GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG
2281  CATAAATTCC GACACCATCG AATGGTGCAA AACCTTTCGC GGTATGGCAT GATAGCGCCC
2341  GGAAGAGAGT CAATTCAGGG TGGTGAATGT GAAACCAGTA ACGTTATACG ATGTCGCAGA
2401  GTATGCCGGT GTCTCTTATC AGACCGTTTC CCGCGTGGTG AACCAGGCCA GCCACGTTTC
2461  TGCGAAAACG CGGGAAAAAG TGGAAGCGGC GATGGCGGAG CTGAATTACA TTCCCAACCG
2521  CGTGGCACAA CAACTGGCGG GCAAACAGTC GTTGCTGATT GGCGTTGCCA CCTCCAGTCT
2581  GGCCCTGCAC GCGCCGTCGC AAATTGTCGC GGCGATTAAA TCTCGCGCCG ATCAACTGGG
2641  TGCCAGCGTG GTGGTGTCGA TGGTAGAACG AAGCGGCGTC GAAGCCTGTA AAGCGGCGGT
2701  GCACAATCTT CTCGCGCAAC GCGTCAGTGG GCTGATCATT AACTATCCGC TGGATGACCA
2761  GGATGCCATT GCTGTGGAAG CTGCCTGCAC TAATGTTCCG GCGTTATTTC TTGATGTCTC
2821  TGACCAGACA CCCATCAACA GTATTATTTT CTCCCATGAA GACGGTACGC GACTGGGCGT
2881  GGAGCATCTG GTCGCATTGG GTCACCAGCA AATCGCGCTG TTAGCGGGCC CATTAAGTTC
2941  TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG GCATAAATAT CTCACTCGCA ATCAAATTCA
3001  GCCGATAGCG GAACGGGAAG GCGACTGGAG TGCCATGTCC GGTTTTCAAC AAACCATGCA
3061  AATGCTGAAT GAGGGCATCG TTCCCACTGC GATGCTGGTT GCCAACGATC AGATGGCGCT
3121  GGGCGCAATG CGCGCCATTA CCGAGTCCGG GCTGCGCGTT GGTGCGGATA TCTCGGTAGT
3181  GGGATACGAC GATACCGAAG ACAGCTCATG TTATATCCCG CCGTTAACCA CCATCAAACA
3241  GGATTTTCGC CTGCTGGGGC AAACCAGCGT GGACCGCTTG CTGCAACTCT CTCAGGGCCA
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3301  GGCGGTGAAG GGCAATCAGC TGTTGCCCGT CTCACTGGTG AAAAGAAAAA CCACCCTGGC
3361  GCCCAATACG CAAACCGCCT CTCCCCGCGC GTTGGCCGAT TCATTAATGC AGCTGGCACG
3421  ACAGGTTTCC CGACTGGAAA GCGGGCAGTG AGCGCAACGC AATTAATGTG AGTTAGCTCA
3481  CTCATTAGGC ACCCCAGGCT TTACACTTTA TGCTTCCGGC TCGTATGTTG TGTGGAATTG
3541  TGAGCGGATA ACAATTTCAC ACAGGAAACA GCTATGACCA TGATTACGGA TTCACTGGCC
3601  GTCGTTTTAC AACGTCGTGA CTGGGAAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA
3661  GCACATCCCC CTTTCGCCAG CTGGCGTAAT AGCGAAGAGG CCCGCACCGA TCGCCCTTCC
3721  CAACAGTTGC GCAGCCTGAA TGGCGAATGG CGCTTTGCCT GGTTTCCGGC ACCAGAAGCG
3781  GTGCCGGAAA GCTGGCTGGA GTGCGATCTT CCTGAGGCCG ATACTGTCGT CGTCCCCTCA
3841  AACTGGCAGA TGCACGGTTA CGATGCGCCC ATCTACACCA ACGTAACCTA TCCCATTACG
3901  GTCAATCCGC CGTTTGTTCC CACGGAGAAT CCGACGGGTT GTTACTCGCT CACATTTAAT
3961  GTTGATGAAA GCTGGCTACA GGAAGGCCAG ACGCGAATTA TTTTTGATGG CGTTGGAATT
4021  AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
4081  GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT
4141  TCTGGATAAT GTTTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC
4201  TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA
4261  CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC
4321  AACCCACTCG ACTTCTTTTG GAATATCTTG AAGAAAAATA TGAAGAGCAT TTGTATGAGC
4381  GCGATGAAGG TGATAAATGG CGAAACAAAA AGTTTGAATT GGGTTTGGAG TTTCCCAATC
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4441  TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA
4501  TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC
4561  TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT
4621  TTGAAACTCT CAAAGTTGAT TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG
4681  ATCGTTTATG TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT
4741  TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA
4801  AATTAGTTTG TTTTAAAAAA CGTATTGAAG CTATCCCACA AATTGATAAG TACTTGAAAT
4861  CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
4921  ATCCTCCAAA ATCGGATCTG ATCGAAGGTC GTGGGATCCC CAGG
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FIG. 28, (SEQ ID NO: 62) ICT1024 N terminus 553 aa coding region: 947-2600

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   1   AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
  61   GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT
 121   TCTGGATAAT GTTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC
 181   TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA
 241   CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC
 301   AACCCACTCG ACTTCTTTTG GAATATCTTG AAGAAAAATA TGAAGAGCAT TTGTATGAGC
 361   GCGATGAAGG TGATAAAATGG CGAAACAAAA AGTTTGAATT GGGTTTGGAG TTTCCCAATC
 421   TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA
 481   TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC
 541   TTGAAGGAGC GGTTTTGGAT ATTAGAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT
 601   TTGAAACTCT CAAAGTTGAT TTTCTTAGCA TATTTAAATG GTGATCATGT GACTTCATGT
 661   ATCGTTTATG TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT
 721   TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCCAAT GTGCCTGGAT GCGTTCCCAA
 781   AATTAGTTTG TTTTAAAAAA CGTATTGAAG CTATCCCACA AATTGATAAG TACTTGAAAT
 841   CCAGCAAGTA TATAGCCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
 901   ATCCTCCAAA ATCGGATCTG ATCGAAGGTC GTGGGATCCC CAGGAATTCC ATGAGTGAGG
 961   CCCGCAGGGA CAGCACGAGC CAGCCTGCAGC GCAAGAAGCC ACCCTGGCTA AAGCTGGACA
1021   TTCCCCTCTGC GGTGCCCCTG ACGGCAGAAG AGCCCAGCTT CCTGCAGCCC CTGAGGGCGAC
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1081  AGGCTTTCCT GAGGAGTGTG AGTATGCCAG CCGAGACAGC CCACATCTCT TCACCCCACC
1141  ATGAGCTCCG GCGGCCGGTG CTGCAACGCC AGACGTCCAT CACACAGACC ATCCGCAGGG
1201  GGACCGCCGA CTGGTTTGGA GTGAGCAAGG ACAGTGACAG CACCCAGAAA TGGCAGCGCA
1261  AGAGCATCCG TCACTGCAGC CAGCGCTACG GGAAGCTGAA GCCCCAGGTC CTCGGGGAGC
1321  TGGACCTGCC CAGCCAGGAC AACGTGTCGC TGACCAGCAC CGAGACGCCA CCCCCACTCT
1381  ACGTGGGGCC ATGCCAGCTG GGCATGCAGA AGATCATAGA CCCCCTGGCC CGTGGCCGTG
1441  CCTTCCGTGT GGCAGATGAC ACTGCGGAAG GCCTGAGTGC CCCACACACT CCCGTCACGC
1501  CGGGTGCTGC CTCCCTCTGC TCCTTCTCCA GCTCCCGCTC AGGTTTCCAC CGGCTCCCGC
1561  GGCGGCGCAA GCGAGAGTCG GTGGCCAAGA TGAGCTTCCG GGCGGCCGCA GCGGCTGATGA
1621  AAGGCCGCTC CGTTAGGGAT GGCACCTTTC GCCGGGCACG GCGTCGAAGC TTCACTCCAG
1681  CTAGCTTTCT GGAGGAGGAC ACAACTGATT TCCCCGATGA GCTGGACACA TCCTTCTTTG
1741  CCCGGGAAGG TATCCTCCAT GAAGAGCTGT CCACATACCC GGATGAAGTT TTCGAGTCCC
1801  CATCGGAGGC AGCGCTAAAG GACTGGGAGA AGGCACCGGA GCAGGCGGAC CTCACCGGCG
1861  GGGCCCTGGA CCGCAGCGAG CTTGAGCGCA GCCACCTGAT GCTGCCCTTG GAGCGGAGGCT
1921  GGCGGAAGCA GAAGGAGGGC GCCGCAGCCC CGCAGCCCAA GGTGCGGCTC CGACAGGAGG
1981  TGGTGAGCAC CGCGGGGCCG CGACGGGCCG AGCGTATCGC GGTGCCGGTG CGCAAGCTCT
2041  TCGCCCGGGA GAAGCGGCCG TATGGGCTGG GCATGGGTGGG ACGGCTCACC AACCGCACCT
2101  ACCGCAAGCG CATCGACAGC TTCGTCAAGC GCCAGATCGA GGACATGGAC GACCACAGGC
2161  CCTTCTTCAC CTACTGGCTT ACCTTCGTGC ACTCGCTCGT CACCATCCTA GCCGTGTGCA
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2221   TCTATGGCAT CGCGCCCGTG GGCTTCTCGC AGCATGAGAC GGTGGACTCG GTGCTGCGGA

2281   ACCGGCGGGT CTACGAGAAC GTCAAGTACG TGCAGCAGGA GAACTTCTGG ATCGGGCCCA

2341   GCTCGGAGGC CCTCATCCAC CTGGGCGCCA AGTTTTCGCC CTGCATGCGC CAGGACCCGC

2401   AGGTGCACAG CTTCATTCGC TCGGCGCGCG AGCGCGGAGAA GCACTCCGCC TGCTGCGTGC

2461   GCAACGACAG GTCGGGCTGC GTGCAGACCT CGGAGGAGGA GTGCTCGTCC ACGCTGGCAG

2521   TGTGGGTGAA GTGGCCCATC CATCCCAGCG CCCCAGAGCT TGCCGGGCCAC AAGAGACAGT

2581   TTGGCTCTGT CTGCCACCAG GATCCCAGGT GAGTCGACTC GAGCGGCCGC ATCGTGACTG

2641   ACTGACGATC TGCCTCGCGC GTTTCGGTGA TGACGGTGAA AACCTCTGAC ACATGCAGCT

2701   CCCGGAGACG GTCACAGCTT GTCTGTAAGC GGATGCCGGG AGCAGACAAG CCCGTCAGGG

2761   CGCGTCAGCG GGTGTTGGCG GGTGTCGGGG CGCAGCCATG ACCCAGTCAC GTAGCGATAG

2821   CGGAGTGTAT AATTCTTGAA GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA

2881   TGTCATGATA ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG

2941   AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA

3001   ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG

3061   TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC

3121   GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT

3181   GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAAACGT TTCCAATGAT

3241   GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG CCGGGCAAGA

3301   GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC
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3361  AGAAAAGCAT  CTTACGGATG  GCATGACAGT  AAGAGAATTA  TGCAGTGCTG  CCATAACCAT
3421  GAGTGATAAC  ACTGCGGCCA  ACTTACTTCT  GACAACGATC  GGAGGACCGA  AGGAGCTAAC
3481  CGCTTTTTTG  CACAACATGG  GGGATCATGT  AACTCGCCTT  GATCGTTGGG  AACCGGAGCT
3541  GAATGAAGCC  ATACCAAACG  ACGAGGGTGA  CACCACGATG  CCTGCAGCAA  TGGCAACAAC
3601  GTTGCGCAAA  CTATTAACTG  GCGAACTACT  TACTCTAGCT  TCCCGGCAAC  AATTAATAGA
3661  CTGGATGGAG  GCGGATAAAG  TTGCAGGACC  ACTTCTGCGC  TCGGCCCTTC  CGGCTGGCTG
3721  GTTTATTGCT  GATAAATCTG  GAGCCGGTGA  GCGTGGGTCT  CGCGGTATCA  TTGCAGCACT
3781  GGGGCCAGAT  GGTAAGCCCT  CCCGTATCGT  AGTTATCTAC  ACGACGGGGA  GTCAGGCAAC
3841  TATGGATGAA  CGAAATAGAC  AGATCGCTGA  GATAGGTGCC  TCACTGATTA  AGCATTGGTA
3901  ACTGTCAGAC  CAAGTTTACT  CATATATACT  TTAGATTGAT  TTAAAACTTC  ATTTTTAATT
3961  TAAAAGGATC  TAGGTGAAGA  TCCTTTTTGA  TAATCTCATG  ACCAAAATCC  CTTAACGTGA
4021  GTTTTCGTTC  CACTGAGCGT  CAGACCCCGT  AGAAAAGATC  AAAGGATCTT  CTTGAGATCC
4081  TTTTTTTCTG  CGCGTAATCT  GCTGCTTGCA  AACAAAAAAA  CCACCGCTAC  CAGCGGTGGT
4141  TTGTTTGCCG  GATCAAGAGC  TACCAACTCT  TTTTCCGAAG  GTAACTGGCT  TCAGCAGAGC
4201  GCAGATACCA  AATACTGTCC  TTCTAGTGTA  GCCGTAGTTA  GGCCACCACT  TCAAGAACTC
4261  TGTAGCACCG  CCTACATACC  TCGCTCTGCT  AATCCTGTTA  CCAGTGGCTG  CTGCCAGTGG
4321  CGATAAGTCG  TGTCTTACCG  GGTTGGACTC  AAGACGATAG  TTACCGGATA  AGGCGCAGCG
4381  GTCGGGCTGA  ACGGGGGGTT  CGTGCACACA  GCCCAGCTTG  GAGCGAACGA  CCTACACCGA
4441  ACTGAGATAC  CTACAGCGTG  AGCTATGAGA  AAGCGCCACG  CTTCCCGAAG  GGAGAAAGGC
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4501  GGACAGGTTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG
4561  GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG
4621  ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT
4681  TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC
4741  TGATTCTGTG GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG
4801  AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCGGAA GAGCGCCTGA TGCGGTATTT
4861  TCTCCTTACG CATCTGTGCG GTATTCACA CCGCATAAAT CCGACACCA TCGAATGGTG
4921  CAAAACCTTT CGCGGTATGG CATGATAGCG CCCGGAAGAG AGTCAATTCA GGGTGGTGAA
4981  TGTGAAACCA GTAACGTTAT ACGATGTCGC AGAGTATGCC GGTGTCTCTT ATCAGACCGT
5041  TTCCCGCGTG GTGAACCAGG CCAGCCACGT TTCTGCGAAA ACGCGGGAAA AAGTGGAAGC
5101  GGCGATGGCG GAGCTGAATT ACATTCCCAA CCGCGTGGCA CAACAACTGG CGGGCAAACA
5161  GTCGTTGCTG ATTGGCGTTG CCACCTCCAG TCTGGCCCTG CACGCGCCGT CGCAAATTGT
5221  CGCGGCGATT AAATCTCGCG CCGATCAACT GGGTGCCAGC GTGGTGGTGT CGATGGTAGA
5281  ACGAAGCGGC GTCGAAGCCT GTAAAGCGGC GGTGCACAAT CTTCTCGCGC AACGCGTCAG
5341  TGGGCTGATC ATTAACTATC CGCTGGATGA CCAGGATGCC ATTGCTGTGG AAGCTGCCTG
5401  CACTAATGTT CCGGCGTTAT TTCTTGATGT CTCTGACCAG ACACCCATCA ACAGTATTAT
5461  TTTCTCCCAT GAAGACGGTA CGCGACTGGG CGTGGAGCAT CTGGTCGCAT TGGGTCACCA
5521  GCAAATCGCG CTGTTAGCGG GCCCATTAAG TTCTGTCTCG GCGCGTCTGC GTCTGGCTGG
5581  CTGGCATAAA TATCTCACTC GCAATCAAAT TCAGCCGATA GCGGAACGGG AAGGCGACTG
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5641  GAGTGCCATG TCCGGTTTTC AACAAACCAT GCAAATGCTG AATGAGGGCA TCGTTCCCAC
5701  TGCGATGCTG GTTGCCAACG ATCAGATGGC GCTGGGCGCA ATGCCGCGCCA TTACCGAGTC
5761  CGGGCTGCGC GTTGGTGCGG ATATCTCGGT AGTGGGATAC GACGATACCG AAGACAGCTC
5821  ATGTTATATC CCGCCGTTAA CCACCATCAA ACAGGATTTT CGCCTGCTGG GGCAAACCAG
5881  CGTGGACCGC TTGCTGCAAC TCTCTCAGGG CCAGGCGGTG AAGGGCAATC AGCTGTTGCC
5941  CGTCTCACTG GTGAAAAGAA AAACCACCCT GGCGCCCAAT ACGCAAACCG CCTCTCCCCG
6001  CGCGTTGGCC GATTCATTAA TGCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA
6061  GTGAGCGCAA CGCAATTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT
6121  TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA
6181  ACAGCTATGA CCATGATTAC GGATTCACTG GCCGTCGTTT TACAACGTCG TGACTGGGAA
6241  AACCCTGGCG TTACCCAACT TAATCGCCTT GCAGCACATC CCCCTTTCGC CAGCTGGCGT
6301  AATAGCGAAG AGGCCCGCAC CGATCGCCCT TCCCAACAGT TGCGCAGCCT GAATGGCGAA
6361  TGGCGCTTTG CCTGGTTTCC GGCACCAGAA GCGGTGCCGG AAAGCTGGCT GGAGTGCGAT
6421  CTTCCTGAGG CCGATACTGT CGTCGTCCCC TCAAACTGGC AGATGCACGG TTACGATGCG
6481  CCCATCTACA CCAACGTAAC CTATCCCATT ACGGTCAATC CGCCGTTTGT TCCCACGGAG
6541  AATCCGACGG GTTGTTACTC GCTCACATTT AATGTTGATG AAAGCTGGCT ACAGGAAGGC
6601  CAGACGCGAA TTATTTTTGA TGGCGTTGGA ATT
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FIG. 29, (SEQ ID NO:64) Coding region for the C terminus 375 aa: 945-2069

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   1   AGCTTATCGA  CTGCACGGTG  CACCAATGCT  TCTGGCGTCA  GGCAGCCATC  GGAAGCTGTG
  61   GTATGGCTGT  GCAGGTCGTA  AATCACTGCA  TAATTCGTGT  CGCTCAAGGC  GCACTCCCGT
 121   TCTGGATAAT  GTTTTTTGCG  CCGACATCAT  AACGGTTCTG  GCAAATATTC  TGAAATGAGC
 181   TGTTGACAAT  TAATCATCGG  CTCGTATAAT  GTGTGGAATT  GTGAGCGGAT  AACAATTTCA
 241   CACAGGAAAC  AGTATTCATG  TCCCCTATAC  TAGGTTATTG  GAAAATTAAG  GGCCTTGTGC
 301   AACCCACTCG  ACTTCTTTTG  GAATATCTTG  AAGAAAAATA  TGAAGAGCAT  TTGTATGAGC
 361   GCGATGAAGG  TGATAAATGG  CGAAACAAAA  AGTTTGAATT  GGGTTTGGAG  TTTCCCAATC
 421   TTCCTTATTA  TATTGATGGT  GATGTTAAAT  TAACACAGTC  TATGGCCATC  ATACGTTATA
 481   TAGCTGACAA  GCACAACATG  TTGGGTGGTT  GTCCAAAAGA  GCGTGCAGAG  ATTTCAATGC
 541   TTGAAGGAGC  GGTTTTGGAT  ATTAGATACG  GTGTTTCGAG  AATTGCATAT  AGTAAAGACT
 601   TTGAAACTCT  CAAAGTTGAT  TTTCTTAGCA  AGCTACCTGA  AATGCTGAAA  ATGTTCGAAG
 661   ATCGTTTATG  TCATAAAACA  TATTTAAAATG  GTGATCATGT  AACCCATCCT  GACTTCATGT
 721   TGTATGACGC  TCTTGATGTT  GTTTTATACA  TGGACCCAAT  GTGCCTGGAT  GCGTTCCCAA
 781   AATTAGTTTG  TTTTAAAAAA  CGTATTGAAG  CTATCCCACA  AATTGATAAG  TACTTGAAAT
 841   CCAGCAAGTA  TATAGCATGG  CCTTTGCAGG  GCTGGCAAGC  CACGTTTGGT  GGTGGCGACC
 901   ATCCTCCAAA  ATCGGATCTG  ATCGAAGGTC  GTGGGATCCC  CAGGAATTCC  CAGGTGCACA
 961   GCTTCATTCG  CTCGGCGCGC  GAGCGCGAGA  AGCACTCCGC  CTGCTGCGTG  CGCAACGACA
1021   GGTCGGGCTG  CGTGCAGACC  TCGGAGGAGG  AGTGCTCGTC  CACGCTGGCA  GTGTGGGTGA
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1081  AGTGGCCCAT CCATCCCAGC GCCCCAGAGC TTGCGGGCCA CAAGAGACAG TTTGGCTCTG
1141  TCTGCCACCA GGATCCCAGG GTGTGTGATG AGCCCTCCTC CGAAGACCCT CATGAGTGGC
1201  CAGAAGACAT CACCAAGTGG CCGATCTGCA CCAAAAACAG CGCTGGGAAC CACACCAACC
1261  ATCCCCACAT GGACTGTGTC ATCACAGGAC GGCCCTGCTG CATTGGCACC AAGGGCAGGT
1321  GTGAGATCAC CTCCCGGGAG TACTGTGACT TCATGAGGGG CTACTTCCAT GAGGAGGCCA
1381  CGCTCTGCTC TCAGGTGCAC TGCATGGATG ATGTGTGTGG GCTCCTGCCT TTTCTCAACC
1441  CCGAGGTGCC TGACCAGTTC TACCGCCTGT GGCTATCCCT CTTCCTGCAC GCCGGGATCT
1501  TGCACTGCCT GGTGTCCATC TGCTTCCAGA TGACTGTCCT GCGGGACCTG GAGAAGCTGG
1561  CAGGCTGGCA CCGCATAGCC ATCATCTACC TGCTGAGTGG TGTCACCGGC AACCTGGCCA
1621  GTGCCATCTT CCTGCCATAC CGAGCAGAGG TGGGTCCCTGC TGGCTCCCAG TTCGGCATCC
1681  TGGCCCTGCCT CTTCGTGGAG CTCTTCCAGA GCTGGCAGAT CCTGGCGCGG CCCTGGCGTG
1741  CCTTCTTCAA GCTGCTGGCT GTGGTGCTCT TCCTCTTCAC CTTTGGGCTG CTGCCGTGGA
1801  TTGACAACTT TGCCCACATC TCGGGGTTCA TCAGTGGCCT CTTCCTCTCC TTCGCCTTCT
1861  TGCCCTACAT CAGCTTTGGC AAGTTCGACC TGTACCGGAA ACGCTGCCAG ATCATCATCT
1921  TTCAGGTGGT CTTCCTGGGC CTCCTGGCTG GCCTGGTGGT CCTCTTCTAC GTCTATCCTG
1981  TCCGCTGTGA GTGGTGTGAG TTCCTCACCT GCATCCCCTT CACTGACAAG TTCTGTGAGA
2041  AGTACGAACT GGAGCGCTCAG CTCCACTGAG TCGACTCGAG CGGCCGCATC GTGACTGACT
2101  GACGATCTGC CTCGCGCGTT TCGGTGATGA CGGTGAAAAC CTCTGACACA TGCAGCTCCC
2161  GGAGACGGTC ACAGCTTGTC TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGCGC
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2221  GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACGTA GCGATAGCGG

2281  AGTGTATAAT TCTTGAAGAC GAAAGGGCCT CGTGATACGC CTATTTTTAT AGGTTAATGT

2341  CATGATAATA ATGGTTTCTT AGACGTCAGG TGGCACTTTT CGGGGAAATG TGCGCGGGAAC

2401  CCCTATTTGT TTATTTTTCT AAATACATTC AAATATGTAT CCGCTCATGA GACAATAAACC

2461  CTGATAAATG CTTCAATAAT ATTGAAAAAG GAAGAGTATG AGTATTCAAC ATTTCCGTGT

2521  CGCCCCTTATT CCCTTTTTTG CGGCATTTTG CCTTCCTGTT TTTGCTCACC CAGAAACGCT

2581  GGTGAAAGTA AAAGATGCTG AAGATCAGTT GGGTGCACGA GTGGGTTACA TCGAACTGGA

2641  TCTCAACAGC GGTAAGATCC TTGAGAGTTT TCGCCCCGAA GAACGTTTTC CAATGATGAG

2701  CACTTTTAAA GTTCTGCTAT GTGGCGCGGT ATTATCCCGT GTTGACGCCG GGCAAGAGCA

2761  ACTCGGTCGC CGCATACACT ATTCTCAGAA TGACTTGGTT GAGTACTCAC CAGTCACAGA

2821  AAAGCATCTT ACGGATGGCA TGACAGTAAG AGAATTATGC AGTGCTGCCA TAACCATGAG

2881  TGATAACACT GCGGCCAACT TACTTCTGAC AACGATCGGA GGACCGAAGG AGCTAACCGC

2941  TTTTTTGCAC AACATGGGGG ATCATGTAAC TCGCCTTGAT CGTTGGGAAC CGGAGCTGAA

3001  TGAAGCCATA CCAAACGACG AGCGTGACAC CACGATGCCT GCAGCAATGG CAACAACGTT

3061  GCGCAAACTA TTAACTGGCG AACTACTTAC TCTAGCTTCC CGGCAACAAT TAATAGACTG

3121  GATGGAGGCG GATAAAGTTG CAGGACCACT TCTGCGCTCG GCCCTTCCGG CTGGCTGGTT

3181  TATTGCTGAT AAATCTGGAG CCGGTGAGCG TGGGTCTCGC GGTATCATTG CAGCACTGGG

3241  GCCAGATGGT AAGCCCTCCC GTATCGTAGT TATCTACACG ACGGGGAGTC AGGCAACTAT

3301  GGATGAACGA AATAGACAGA TCGCTGAGAT AGGTGCCTCA CTGATTAAGC ATTGGTAACT
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3361  GTCAGACCAA GTTTACTCAT ATATACTTTA GATTGATTTA AAACTTCATT TTTAATTTAA
3421  AAGGATCTAG GTGAAGATCC TTTTTGATAA TCTCATGACC AAAATCCCTT AACGTGAGTT
3481  TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA AAAGATCAAA GGATCTTCTT GAGATCCTTT
3541  TTTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAAACCA CCGCTACCAG CGGTGGTTTG
3601  TTTGCCGGAT CAAGAGCTAC CAACTCTTTT TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA
3661  GATACCAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTAGGC CACCACTTCA AGAACTCTGT
3721  AGCACCGCCT ACATACCTCG CTCTGCTAAT CCTGTTACCA GTGGCTGCTG CCAGTGGCGA
3781  TAAGTCGTGT CTTACCGGGT TGGACTCAAG ACGATAGTTA CCGGATAAGG CGCAGCGGTC
3841  GGGCTGAACG GGGGGTTCGT GCACACAGCC CAGCTTGGAG CGAACGACCT ACACCGAACT
3901  GAGATACCTA CAGCGTGAGC TATGAGAAAG CGCCACGCTT CCCGAAGGGA GAAAGGCGGA
3961  CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG
4021  AAACGCCTGG TATCTTTATA GTCCTGTCGG GTTTCGCCAC CTCTGACTTG AGCGTCGATT
4081  TTTGTGATGC TCGTCAGGGG GGCGGAGCCT ATGGAAAAAC GCCAGCAACG CGGCCTTTTT
4141  ACGGTTCCTG GCCTTTTGCT GGCCTTTTGC TCACATGTTC TTTCCTGCGT TATCCCCTGA
4201  TTCTGTGGAT AACCGTATTA CCGCCTTTGA GTGAGCTGAT ACCGCTCGCC GCAGCCGAAC
4261  GACCGAGCGC AGCGAGTCAG TGAGCGAGGA AGCGGAAGAG CGCCTGATGC GGTATTTTCT
4321  CCTTACGCAT CTGTGCGGTA TTTCACACCG CATAAATTCC GACACCATCG AATGGTGCAA
4381  AACCTTTCGC GGTATGGCAT GATAGCGCCC GGAAGAGAGT CAATTCAGGG TGGTGAATGT
4441  GAAACCAGTA ACGTTATACG ATGTCGCAGA GTATGCCGGT GTCTCTTATC AGACCGTTTC
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4501  CCGCGTGGTG AACCAGGCCA GCCACGTTTC TGCGAAAACG CGGGAAAAAG TGGAAGCGGC
4561  GATGGCGGAG CTGAATTACA TTCCCAACCG CGTGGCACAA CAACTGGCGG GCAAACAGTC
4621  GTTGCTGATT GGCGGTTGCCA CCTCCAGTCT GGCCCTGCAC GCGCCGTCGC AAATTGTCGC
4681  GGCGATTAAA TCTCGCGCCG ATCAACTGGG TGCCAGCGTG GTGGTGTCGA TGGTAGAACG
4741  AAGCGGCGTC GAAGCCTGTA AAGCGGCGGT GCACAATCTT CTCGCGCAAC GCGTCAGTGG
4801  GCTGATCATT AACTATCCGC TGGATGACCA GGATGCCATT GCTGTGGAAG CTGCCTGCAC
4861  TAATGTTCCG GCGTTATTTC TTGATGTCTC CCCATCAACA GTATTATTTT
4921  CTCCCATGAA GACGGTACGC GACTGGGCGT GGAGCATCTG GTCGCATTGG GTCACCAGCA
4981  AATCGCGCTG TTAGCGGGCC CATTAAGTTC TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG
5041  GCATAAATAT CTCACTCGCA ATCAAATTCA GCCGATAGCG GAACGGGAAG GCGACTGGAG
5101  TGCCATGTCC GGTTTTCAAC AAACCATGCA AATGCTGAAT GAGGGCATCG TTCCCACTGC
5161  GATGCTGGTT GCCAACGATC AGATGGCGCT GGGCGCAATG CGGCGCCATTA CCGAGTCCGG
5221  GCTGCGCGTT GGTGCGGATA TCTCGGTAGT GGGATACGAC GATACCGAAG ACAGCTCATG
5281  TTATATCCCG CCGTTAACCA CCATCAAACA GGATTTTCGC CTGCTGGGGC AAACCAGCGT
5341  GGACCGCTTG CTGCAACTCT CTCAGGGCCA GGCGGGTGAAG GGCAATCAGC TGTTGCCCGT
5401  CTCACTGGTG AAAAGAAAAA CCACCCTGGC GCCCAATACG CAAACCGCCT CTCCCCGCGC
5461  GTTGGCCGAT TCATTAATGC AGCTGGCACG ACAGGTTTCC CGACTGGAAA GCGGGCAGTG
5521  AGCGCAACGC AATTAATGTG AGTTAGCTCA CTCATTAGGC ACCCCAGGCT TTACACTTTA
5581  TGCTTCCGGC TCGTATGTTG TGTGGAATTG TGAGCGGATA ACAATTTCAC ACAGGAAACA
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5641  GCTATGACCA TGATTACGGA TTCACTGGCC GTCGTTTTAC AACGTCGTGA CTGGGAAAAC
5701  CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG CTGGCGTAAT
5761  AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA TGGCGAATGG
5821  CGCTTTGCCT GGTTTCCGGC ACCAGAAGCG GTGCCGGAAA GCTGGCTGGA GTGCGATCTT
5881  CCTGAGGCCG ATACTGTCGT CGTCCCCTCA AACTGGCAGA TGCACGGTTA CGATGCGCCC
5941  ATCTACACCA ACGTAACCTA TCCCATTACG GTCAATCCGC CGTTTGTTCC CACGGAGAAT
6001  CCGACGGGTT GTTACTCGCT CACATTTAAT GTTGATGAAA GCTGGCTACA GGAAGGCCAG
6061  ACGCGAATTA TTTTTGATGG CGTTGGAATT
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FIG. 30, (SEQ ID NO:66) ICT1024 coding region: 310-2879

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   1  TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT
  61  TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG GGCCTCTTCG
 121  CTATTACGCC AGCTTGGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGTAACGCCA
 181  GGGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG ATTGGCTAGC
 241  AGAATAAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGGAGCTCGT
 301  GGATCCGAAT TCCATGAGTG AGGCCCGCAG GGACAGCACG AGCAGCCTGC AGCGCAAGAA
 361  GCCACCCTGG CTAAAGCTGG ACATTCCCTC TGCGGGTGCCC CTGACGGGCAG AAGAGCCCAG
 421  CTTCCTGCAG CCCCTGAGGC GACAGGGCTTT CCTGAGGAGT GTGAGTATGC CAGCCGAGAC
 481  AGCCCACATC TCTTCACCCC ACCATGAGCT CCGGCGGCCG GTGCTGCAAC GCCAGACGTC
 541  CATCACACAG ACCATCCGCA GGGGGGACCGC CGACTGGTTT GGAGTGAGCA AGGACAGTGA
 601  CAGCACCCAG AAATGGCAGC GCAAGAGAGCAT CCGTCACTGC AGCCAGCGCT ACGGGAAGCT
 661  GAAGCCCCAG GTCCTCCGGGG AGCTGGACCT GCCCAGCCAG GACAACGTGT CGCTGACCAG
 721  CACCGAGACG GCCCGGTGGCC TCTACGTGGG GCCATGCCAG CTGGGGCATGC AGAAGATCAT
 781  AGACCCCCTG GCCCGGTGGCC GTGCCTTCCG TGTGGCAGAT GACACTGCGG AAGGCCTGAG
 841  TGCCCCACAC ACTCCCGTCA CGCCGGGCTGC CGCGGCGGCG CAAGCGAGAG TCGGTGGCCA AGATGAGCTT
 901  CTCAGGTTTC CACCGGCTCC CGCGGCGGCG GCAGCGGCTGA TGAAAGGCCCG CTCCGTTAGG GATGGCACCT TTCGCCGGGC
 961  CCGGGGCGCC GCAGCGGCTGA TGAAAGGCCCG CTCCGTTAGG GATGGCACCT TTCGCCGGGC
1021  ACGGGCGTCGA AGCTTCACTC CAGCTAGCTT TCTGGAGGAG GACACAACTG ATTTCCCCGA
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1081  TGAGCTGGAC  ACATCCTTCT  TTGCCCGGGA  AGTGTATCCT  CATGAAGAGC  TGTCCACATA
1141  CCCGGATGAA  GTTTTCGAGT  CCCCATCGGA  GGCAGCGCTA  AAGGACTGGG  AGAAGGCACC
1201  GGAGCAGGCG  GACCTCACCG  GCGGGGCCCT  GGACCGCAGC  GAGCTTGAGC  GCAGCCACCT
1261  GATGCTGCCC  TTGGAGCGAG  GCTGGCGGAA  GCAGAAGGAG  GGCGCCGGCA  CCCCGCAGCC
1321  CAAGGTGCGG  CTCCGACAGG  AGGTGGTGAG  CACCGCGGGG  CCGCGACGGG  GCCAGCGTAT
1381  CGCGGTGCCG  GTGCGCAAGC  TCTTCGCCCG  GGAGAAGCGG  CCGTATGGGC  TGGGCATGGT
1441  GGGACGGCTC  ACCAACCGCA  CCTACCGCAA  GCGCATCGAC  AGCTTCGTCA  AGCGCCAGAT
1501  CGAGGACATG  GACGACCACA  GGCCCTTCTT  CACCTACTGG  CTTACCTTCG  TGCACTCGCT
1561  CGTCACCATC  CTAGCCGTGT  GCATCTATGG  CATCGCGCCC  GTGGGCTTCT  CGCAGCATGA
1621  GACGGTGGAC  TCGGTGCTGC  GGAACCGCGG  GGTCTACGAG  AACGTCAAGT  ACGTGCAGCA
1681  GGAGAACTTC  TGGATCGGGC  CCAGCTCGGA  GGCCCTCATC  CACCTGGGCG  CCAAGTTTTC
1741  GCCCTGCATG  CGCCAGGACC  CGCAGGTGCA  CAGCTTCATT  CGCTCGGCGC  GCGAGCGCGA
1801  GAAGCACTCC  GCCTGCTGCG  TGCGCAACGA  CAGGTCGGGC  TGCGTGCAGA  CCTCGGAGGA
1861  GGAGTGCTCG  TCCACGCTGG  CAGTGTGGGT  GAAGTGGCCC  ATCCATCCCA  GCGCCCCAGA
1921  GCTTGCGGGC  CACAAGAGAC  AGTTTGGCTC  TGTCTGCCAC  CAGGATCCCA  GGGTGTGTGA
1981  TGAGCCCTCC  TCCGAAGACC  CTCATGAGTG  GCCAGAAGAC  ATCACCAAGT  GGCCGATCTG
2041  CACCAAAAAC  AGCGCTGGGA  ACCACACCAA  CCATCCCCAC  ATGGACTGTG  TCATCACAGG
2101  ACGGCCCTGC  TGCATTGGCA  CCAAGGGCAG  GTGTGAGATC  ACCTCCCGGG  AGTACTGTGA
2161  CTTCATGAGG  GGCTACTTCC  ATGAGGAGGC  CACGCTCTGC  TCTCAGGTGC  ACTGCATGGA
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2221  TGATGTGTGT GGGCTCCTGC CTTTTCTCAA CCCCGAGGTG CCTGACCAGT TCTACCGCCT
2281  GTGGCTATCC CTCTTCCTGC ACGCCGGGAT CTTGCACTGC CTGGTGTCCA TCTGCTTCCA
2341  GATGACTGTC CTGCGGGACC TGGAGAAGCT GGCAGGCTGG CACCGCATAG CCATCATCTA
2401  CCTGCTGAGT GGTGTCACCG GCAACCTGGC CAGTGCCATC TTCCTGCCAT ACCGAGCAGA
2461  GGTGGGTCCT GCTGGCTCCC AGTTCGGCAT CCTGGCCTGC CTCTTCGTGG AGCTCTTCCA
2521  GAGCTGGCAG ATCCTGGCGC GGCCCTGGCG TGCCTTCTTC AAGCTGCTGG CTGTGGTGCT
2581  CTTCCTCTTC ACCTTTGGGC TGCTGCCGTG GATTGACAAC TTTGCCCACA TCTCGGGGTT
2641  CATCAGTGGC CTCTTCCTCT CCTTGCCCTT CTTGCCCTAC ATCAGCTTTG GCAAGTTCGA
2701  CCTGTACCGG AAACGCTGCC AGATCATCAT CTTTCAGGTG GTCTTCCTGG GCCTCCTGGC
2761  TGGCCTGGTG GTCCTCTTCT ACGTCTATCC TGTCCGCTGT GAGTGGTGTG AGTTCCTCAC
2821  CTGCATCCCC TTCACTGACA AGTTCTGTGA GAAGTACGAA CTGGACGCTC AGCTCCACAT
2881  CGATACGCGT TCGAAGCTTG CGGCCGCACA GCTGTATACA CGTGCAAGCC AGCCAGAACT
2941  CGCTCCTGAA GACCCAGAGG ATCTCGAGCA CCACCACCAC CACCACTAAT GTTAATTAAG
3001  TTGGGGCGTTG TAATCATAGT CATAATCAAT ACTCCTGACT GCGGTAGCAA TTTAACTGTG
3061  ATAAACTACC GCATTAAAGC TATTCGATGA TAAGCTGTCA AACATGATAA TTCTTGAAGA
3121  CGAAAGGGCC TAGGCTGATA AAACAGAATT TGCCTGGCGG CAGTAGCGCG GTGGTCCCAC
3181  CTGACCCCAT GCCGAACTCA GAAGTGAAAC GCCGTAGCGC CGATGGTAGT GTGGGGTCTC
3241  CCCATGCGAG AGTAGGGAAC TGCCAGGCAT CAAATAAAAC GAAAGGCTCA GTCGAAAGAC
3301  TGGGCCTTTC GTTTTATCTG TTGTTTGTCG GTGAACGCTC TCCTGAGTAG GACAAATCCG
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3361  CCGGGGAGCGG  ATTTGAACGT  TGCGAAGCAA  CGGCCCGGAG  GGTGGCGGGC  AGGACGCCCG
3421  CCATAAACTG   CCAGGCATCA  AATTAAGCAG  AAGGCCATCC  TGACGGATGG  CCTTTTTGCG
3481  TTTCTACAAA   CTCTTTTGTT  TATTTTTCTA  AATACATTCA  AATATGTATC  CGCTGAGCAA
3541  TAACTAGCAT   AACCCCTTGG  GGCCTCTAAA  CGGGTCTTGA  GGGGTTTTTT  GCTGAAAGGA
3601  GGAACTATAT   CCGGATTGGC  GAATGGGACG  CGCCCTGTAG  CGGCGCATTA  AGCGCGGCGG
3661  GTGTGGTGGT   TACGCGCAGC  GTGACCGCTA  CACTTGCCAG  CGCCCTAGCG  CCCGCTCCTT
3721  TCGCTTTCTT   CCCTTCCTTT  CTCGCCACGT  TCGCCGGCTT  TCCCCGTCAA  GCTCTAAATC
3781  GGGGGCTCCC   TTTAGGGTTC  CGATTTAGTG  CTTTACGGCA  CCTCGACCCC  AAAAAACTTG
3841  ATTAGGGTGA   TGGTTCACGT  AGTGGGCCAT  CGCCCTGATA  GACGGTTTTT  CGCCCTTTGA
3901  CGTTGGGAGTC  CACGTTCTTT  AATAGTGGAC  TCTTGTTCCA  AACTGGAACA  ACACTCAACC
3961  CTATCTCGGT   CTATTCTTTT  GATTATTAAG  GGATTTTGCC  GATTTCGGCC  TATTGGTTAA
4021  AAAAATGAGCT  GATTTAACAA  AAATTTAAACG CGAATTTTAA  CAAAATATTA  ACGTTTACAA
4081  TTTCTGGCGG   CACGATGGCA  TGAGATTATC  AAAAAGGATC  TTCACCTAGA  TCCTTTTAAA
4141  TTAAAAATGA   AGTTTTAAAT  CAATCTAAAG  TATATATGAG  TAAACTTGGT  CTGACAGTTA
4201  CCAATGCTTA   ATCAGTGAGG  CACCTATCTC  AGCGATCTGT  CTATTTCGTT  CATCCATAGT
4261  TGCCTGACTC   CCCGTCGTGT  AGATAACTAC  GATACGGGAG  GGCTTACCAT  CTGGCCCCAG
4321  TGCTGCAATG   ATACCGCGAG  ACCCACGCTC  ACCGGCTCCA  GATTTATCAG  CAATAAACCA
4381  GCCAGCCGGA   AGGGCCGAGC  GCAGAAGTGG  TCCTGCAACT  TTATCCGCCT  CCATCCAGTC
4441  TATTAATTGT   TGCCGGGAAG  CTAGAGTAAG  TAGTTCGCCA  GTTAATAGTT  TGCGCAACGT
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4501  TGTTGCCATT GCTACAGGCA TCGTGGTGTC ACGGCTCGTC GTTTGGTATGG CTTCATTCAG
4561  CTCCGGTTCC CAACGATCAA GGCGGAGTTA CATGATCCCC ATGTTGTGCA AAAAAGCGGT
4621  TAGCTCCTTC GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG GCCGCAGTGT TATCACTCAT
4681  GGTTATGGCA GCACTGCATA ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT
4741  GACTGGTGAG TACTTCAACC AAGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC
4801  TTGCCCGGCG TCAATACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT
4861  CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC TTACCGCTGT TGAGATCCAG
4921  TTCGATGTAA CCCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT
4981  TTCTGGGTGA GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG
5041  GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATCATGA CCAAAATCCC TTAACGTGAG
5101  TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT
5161  TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGTT
5221  TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG
5281  CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT
5341  GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC
5401  GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG
5461  TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA
5521  CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG
5581  GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG
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5641  GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA
5701  TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT
5761  TTACGGTTCC TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT
5821  GATTCTGTGG ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA
5881  ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCCGGCG ATAATGGCCT GCTTCTCGCC
5941  GAAACGTTTG GTGGCGGGAC CAGTGACGAA GGCTTGAGCG AGGGCGTGCA AGATTCCGAA
6001  TACCGCAAGC GACAGGCCGA TCATCGTCGC GCTCCAGCGA AAGCGGTCCT CGCCGAAAAT
6061  GACCCAGAGC GCTGCCGGCA CCTGTCCTAC GAGTTGCATG ATAAAGAAGA CAGTCATAAG
6121  TGCGGCGACG ACCGGTGAAT TGTGAGCGCT CACAATTCTC GTGACATCAT AACGTCCCGC
6181  GAAAT
```

FIG. 31. (SEQ ID NO:68) Coding region for the N terminus 400 aa of ICT1024: 314-1515

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   1  TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT
  61  TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG GGCCTCTTCG
 121  CTATTACGCC AGCTTGGCAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGTAACGCCA
 181  GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG ATTGGCTAGC
 241  AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGGAGCTCGT
 301  GGATCCGAAT TCCATGAGTG AGGCCCGCAG GGACAGCACG AGCAGCCTGC AGCGCAAGAA
 361  GCCACCCTGG CTAAAGCTGG ACATTCCCTC TGCGGTGCCC CTGACGGCAG AAGAGCCCAG
 421  CTTCCTGCAG CCCCTGAGGC GACAGGCTTT CCTGAGGAGT GTGAGTATGC CAGCCGAGAC
 481  AGCCCACATC TCTTCACCCC ACCATGAGCT CCGGCGGCCG GTGCTGCAAC GCCAGACGTC
 541  CATCACACAG ACCATCCCGCA GGGGGACCGC CGACTGGTTT GGAGTGAGCA AGGACAGTGA
 601  CAGCACCCAG AAATGGCAGC GCAAGAGCAT CCGTCACTGC AGCCAGCGCT ACGGGAAGCT
 661  GAAGCCCCAG GTCCTCCGGG AGCTGGACCT GCCCAGCCAG GACAACGTGT CGCTGACCAG
 721  CACCGAGACG CCACCCCCAC TCTACGGTGGG GCCATGCCAG CTGGGCATGC AGAAGATCAT
 781  AGACCCCCTG GCCCGTGGCC GTGCCTTCCG TGTGGCAGAT GACACTGCGG AAGGCCTGAG
 841  TGCCCACAC ACTCCCGTCA CGCCGGGTGC TGCCTCCCTC TGCTCCTTCT CCAGCTCCCG
 901  CTCAGGTTTC CACCGGCTCC CGCGGCGGCG CAAGCGAGAG TCGGTGGCCA AGATGAGCTT
 961  CCGGGGCGGCC GCAGCGCTGA TGAAAGGCCG CTCCGTTAGG GATGGCCACCT TTCGCGGGGC
1021  ACGGCGTGA AGCTTCACTC CAGCTAGCTT TCTGGAGGAG GACACAACTG ATTTCCCGA
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1081  TGAGCTGGAC ACATCCTTCT TTGCCCGGGA AGGTATCCTC CATGAAGAGC TGTCCACATA
1141  CCCGGATGAA GTTTTCGAGT CCCATCGGA  GGCAGCGCTA AAGGACTGGG AGAAGGCACC
1201  GGAGCAGGCG GACCTCCACCG GCGGGGCCCT GAGCTTGAGC GGACCGCAGC GCAGCCACCT
1261  GATGCTGCCC TTGGAGCGAG GCTGGCGGAA GCAGAAGGAG GGCGCCGCAG CCCCGCAGCC
1321  CAAGGTGCGG CTCCGACAGG AGGTGGTGAG CACCGCGGGG CCGCCGACGGG GCCAGCGTAT
1381  CGCGGTGCCG GTGCGCCAAGC TCTTCGCCCG GGAGAAGCGG CCGTATGGGC TGGGCATGGT
1441  GGGACGGCTC ACCAACCGCA CCTACCGCAA GCGCATCGAC AGCTTCGTCA AGCGCCAGAT
1501  CGAGGACATG GACATCGATA CGCGTTCGAA GCTTGCGGCC GCACAGCTGT ATACACGTGC
1561  AAGCCAGCCA GAACTCGCTC CTGAAGACCC AGAGGATCTC GAGCACCACC ACCACCACCA
1621  CTAATGTTAA TTAAGTTGGG CGTTGTAATC ATAGTCATAA TCAATACTCC TGACTGCGTT
1681  AGCAATTTAA CTGTGATAAA CTACCGCATT AAAGCTATTC GATGATAAGC TGTCAAACAT
1741  GATAATTCTT GAAGACGAAA GGGCCTAGGC TGATAAAACA GAATTTGCCT GGCGGCAGTA
1801  GCGCGGTGGT CCCACCTGAC CCCATGCCGA ACTCAGAAGT GAAACGCCGT AGCGCCGATG
1861  GTAGTGTGGG GTCTCCCCAT GCGAGAGTAG GGAACTGCCA GGCATCAAAT AAAACGAAAG
1921  GCTCAGTCGA AAGACTGGGC CTTTCGTTTT ATCTGTTGTT TGTCGGTGAA CGCTCTCCTG
1981  AGTAGGACAA ATCCGCCGGG AGCGGATTTG AACGTTGCGA AGCAACGGCC CGGAGGGTGG
2041  CGGGCAGGAC GCCCGCCATA AACTGCCAGG CATCAAATTA AGCAGAAGGC CATCCTGACG
2101  GATGGCCTTT TTGCGTTTCT ACAAACTCTT TTGTTTATTT TTCTAAATAC ATTCAAATAT
2161  GTATCCGCTG AGCAATAACT AGCATAACCC CTTGGGGGCCT CTAAACGGGT CTTGAGGGGT
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2221  TTTTTGCTGA AAGGAGGAAC TATATCCGGA TTGGCGAATG GGACGCGCCC TGTAGCGGCG
2281  CATTAAGCGC GGCGGGTGTG GTGGTTACGC GCAGCGTGAC CGCTACACTT GCCAGCGCCC
2341  TAGCGCCCGC TCCTTTCGCT TTCTTCCCTT CCTTTCTCGC CACGTTCGCC GGCTTTCCCC
2401  GTCAAGCTCT AAATCGGGGG CTCCCTTTAG GGTTCCGATT TAGTGCTTTA CGGCACCTCG
2461  ACCCCAAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC TGATAGACGG
2521  TTTTTCGCCC TTTGACGTTG GAGTCCACGT TCTTTAATAG TGGACTCTTG TTCCAAACTG
2581  GAACAACACT CAACCCTATC TCGGTCTATT CTTTTGATTT ATAAGGGATT TTGCCGATTT
2641  CGGCCTATTG GTTAAAAAAT GAGCTGATTT AACAAAAATT TAACGCGAAT TTTAACAAAA
2701  TATTAACGTT TACAATTTCT GGCGGCACGA TGGCATGAGA TTATCAAAAA GGATCTTCAC
2761  CTAGATCCTT TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC
2821  TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT
2881  TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT
2941  ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCCAGATTT
3001  ATCAGCAATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC
3061  CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA
3121  TAGTTTGCGC AACGTTGTTG CCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTTGG
3181  TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT
3241  GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC
3301  AGTGTTATCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT
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3361  AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG
3421  GCGACCGAGT TGCTCTTGCC CGGCGTCAAT ACGGGATAAT ACCGCGCCAC ATAGCAGAAC
3481  TTTAAAAGTG CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACTCTCAA GGATCTTACC
3541  GCTGTTGAGA TCCAGTTCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT
3601  TACTTTCACC AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG
3661  AATAAGGGCG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT CATGACCAAA
3721  ATCCCTTAAC GTGAGTTTTC GTTCCACTGA GCGTCAGACC CCGTAGAAAA GATCAAAGGA
3781  TCTTCTTGAG ATCCTTTTTT TCTGCGCGTA ATCTGCTGCT TGCAAACAAA AAAACCACCG
3841  CTACCAGCGG TGGTTTGTTT GCCGGATCAA GAGCTACCAA CTCTTTTTCC GAAGGTAACT
3901  GGCTTCAGCA GAGCGCAGAT ACCAAATACT GTCCTTCTAG TGTAGCCGTA GTTAGGCCAC
3961  CACTTCAAGA ACTCTGTAGC ACCGCCTACA TACCTCGCTC TGCTAATCCT GTTACCAGTG
4021  GCTGCTGCCA GTGGCGATAA GTCGTGTCTT ACCGGGTTGG ACTCAAGACG ATAGTTACCG
4081  GATAAGGCGC AGCGGTCGGG CTGAACGGGG GGTTCGTGCA CACAGCCCAG CTTGGAGCGA
4141  ACGACCTACA CCGAACTGAG ATACCTACAG CGTGAGCTAT GAGAAAGCGC CACGCTTCCC
4201  GAAGGGAGAA AGGCGGACAG GTATCCGGTA AGCGGCAGGG TCGGAACAGG AGAGCGCACG
4261  AGGGAGCTTC CAGGGGGAAA CGCCTGGTAT CTTTATAGTC CTGTCGGGTT TCGCCACCTC
4321  TGACTTGAGC GTCGATTTTT GTGATGCTCG TCAGGGGGGC GGAGCCTATG GAAAAACGCC
4381  AGCAACGCGG CCTTTTTACG GTTCCTGGCC TTTTGCTGGC CTTTTGCTCA CATGTTCTTT
4441  CCTGCGTTAT CCCCTGATTC TGTGGATAAC CGTATTACCG CCTTTGAGTG AGCTGATACC
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4501  GCTCGCCGCA GCCGAACGAC CGAGCGCAGC GAGTCAGTGA GCGAGGAAGC CGGCGATAAT
4561  GGCCTGCTTC TCGCCGAAAC GTTTGGTGGC GGGACCAGTG ACGAAGGCTT GAGCGAGGGC
4621  GTGCAAGATT CCGAATACCG CAAGCGACAG GCCGATCATC GTCGCGCTCC AGCGAAAGCG
4681  GTCCTCGCCG AAAATGACCC AGAGCGCTGC CGGCACCTGT CCTACGAGTT GCATGATAAA
4741  GAAGACAGTC ATAAGTGCGG CGACGACCGG TGAATTGTGA GCGGCTCACAA TTCTCGTGAC
4801  ATCATAACGT CCCGGCGAAAT
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FIG. 32. (SEQ ID NO 69) Coding region for the C terminus 373 aa of ICT1024: 308-1431

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   1  TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT

  61  TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG GGCCTCTTCG

 121  CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGTAACGCCA

 181  GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG ATTGGCTAGC

 241  AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGGAGCTCGT

 301  GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG AGAAGCACTC

 361  CGCCTGCTGC GTGCGCAACG ACAGGTCGGG CTGCGTGCAG ACCTCGGAGG AGGAGTGCTC

 421  GTCCACGCTG GCAGTGTGGG TGAAGTGGCC CATCCATCCC AGCGCCCCAG AGCTTGCGGG

 481  CCACAAGAGA CAGTTTGGCT CTGTCTGCCA CCAGGATCCC AGGGTGTGTG ATGAGCCCTC

 541  CTCCGAAGAC CCTCATGAGT GGCCAGAGA CATCACCAAG TGGCCGATCT GCACCAAAAA

 601  CAGCGGCTGGG AACCACACCA ACCATCCCCA CATGGACTGT GTCATCACAG GACGGCCCTG

 661  CTGCATTGGC ACCAAGGGCA GGTGTGAGAT CACCTCCCGG GAGTACTGTG ACTTCATGAG

 721  GGGCTACTTC CATGAGGAGG CCACGCTCTG CTCTCAGGTG CACTGGCATGG ATGATGTGTG

 781  TGGGCTCCTG CCTTTTCTCA ACCCCGAGGT GCCTGACCAG TTCTACCGCC TGTGGCTATC

 841  CCTCTTCCTG CACGCCGGGA TCTTGCACTG CCTGGTGTCC ATCTGCTTCC AGATGACTGT

 901  CCTGCGGGAC CTGGAGAAGC TGGCAGGCTG GCACCGCCATA GCCATCATCT ACCTGCTGAG

 961  TGGTGTCACC GGCAACCTGG CCAGTGCCAT CTTCCTGCCA TACCGAGCAG AGGTGGGTCC

1021  TGCTGGCTCC CAGTTCGGCA TCCTGGCCTG CCTCTTCGTG GAGCTCTTCC AGAGCTGGCA
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1081  GATCCCTGGCG  CGGCCCTGGC  GTGCCCTTCTT  CAAGCTGCTG  GCTGTGGTGC  TCTTCCTCTT
1141  CACCTTTGGG   CTGCTGCCGT  GGATTGACAA   CTTTGCCCAC  ATCTCGGGGT  TCATCAGTGG
1201  CCTCTTCCTC   TCCTTCGCCT  TCTTGCCCTA   CATCAGCTTT  GGCAAGTTCG  ACCTGTACCG
1261  GAAACGCTGC   CAGATCATCA  TCTTTCAGGT   GGTCTTCCTG  GGCCTCCTGG  CTGGCCTGGT
1321  GGTCCTCTTC   TACGTCTATC  CTGTCCGCTG   TGAGTGGTGT  GAGTTCCTCA  CCTGCATCCC
1381  CTTCACTGAC   AAGTTCTGTG  AGAAGTACGA   ACTGGACGCT  CAGCTCCACA  TCGATACGCG
1441  TTCGAAGCTT   GCGGCCGCAC  AGCTGTATAC   ACGTGCAAGC  CAGCCAGAAC  TCGCTCCTGA
1501  AGACCCAGAG   GATCTCGAGC  ACCACCACCA   CCACCACTAA  TGTTAATTAA  GTTGGGCGTT
1561  GTAATCATAG   TCATAATCAA  TACTCCTGAC   TGCGTTAGCA  ATTTAACTGT  GATAAACTAC
1621  CGCATTAAAG   CTATTCGATG  ATAAGCTGTC   AAACATGATA  ATTCTTGAAG  ACGAAAGGGC
1681  CTAGGCTGAT   AAAACAGAAT  TTGCCTGGCG   GCAGTAGCGC  GGTGGTCCCA  CCTGACCCCA
1741  TGCCGAACTC   AGAAGTGAAA  CGCCGTAGCG   CCGATGGTAG  TGTGGGGTCT  CCCCATGCGA
1801  GAGTAGGGAA   CTGCCAGGAA  TCAAATAAAA   CGAAAGGCTC  AGTCGAAAGA  CTGGGCCTTT
1861  CGTTTTATCT   GTTGTTTGTC  GGTGAACGCT   CTCCTGAGTA  GGACAAATCC  GCCGGGAGCG
1921  GATTTGAACG   TTGCGAAGCA  ACGGCCCGGA   GGGTGGCGGG  CAGGACGCCC  GCCATAAACT
1981  GCCAGGCATC   AAATTAAGCA  GAAGGCCATC   CTGACGGATG  GCCTTTTTGC  GTTTCTACAA
2041  ACTCTTTTGT   TTATTTTTCT  AAATACATTC   AAATATGTAT  CCGCTCATGA  ATAACTAGCA
2101  TAACCCCTTG   GGGCCTCTAA  ACGGGTCTTG   AGGGGTTTTT  TGCTGAAAGG  AGGAACTATA
2161  TCCGGATTGG   CGAATGGGAC  GCGCCCTGTA   GCGGCGCATT  AAGCGCGGCG  GGTGTGGTGG
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2221  TTACGCGCAG  CGTGACCGCT  ACACTTGCCA  GCGCCCTAGC  GCCCGCTCCT  TTCGCTTTCT
2281  TCCCTTCCTT  TCTCGCCACG  TTCGCCGGCT  TTCCCCGTCA  AGCTCTAAAT  CGGGGGCTCC
2341  CTTTAGGGTT  CCGATTTAGT  GCTTTACGGC  ACCTCGACCC  CAAAAAACTT  GATTAGGGTG
2401  ATGGTTCACG  TAGTGGGCCA  TCGCCCTGAT  AGACGGTTTT  TCGCCCTTTG  ACGTTGGAGT
2461  CCACGTTCTT  TAATAGTGGA  CTCTTGTTCC  AAACTGGAAC  AACACTCAAC  CCTATCTCGG
2521  TCTATTCTTT  TGATTTATAA  GGGATTTTGC  CGATTTCGGC  CTATTGGTTA  AAAAATGAGC
2581  TGATTTAACA  AAAATTTAAC  GCGGAATTTA  ACAAAATATT  AACGTTTACA  ATTTCTGGCG
2641  GCACGATGGC  ATGAGATTAT  CAAAAAGGAT  CTTCACCTAG  ATCCTTTTAA  ATTAAAAATG
2701  AAGTTTTAAA  TCAATCTAAA  GTATATATGA  GTAAACTTGG  TCTGACAGTT  ACCAATGCTT
2761  AATCAGTGAG  GCACCTATCT  CAGCGGATCT  TCTATTTCGT  TCATCCATAG  TTGCCTGACT
2821  CCCCGTCGTG  TAGATAACTA  CGATACGGGA  GGGCTTACCA  TCTGGCCCCA  GTGCTGCAAT
2881  GATACCGCGA  GACCCACGCT  CACCGGCTCC  AGATTTATCA  GCAATAAACC  AGCCAGCCGG
2941  AAGGGCCGAG  CGCAGAAGTG  GTCCTGCAAC  TTTATCCGCC  TCCATCCAGT  CTATTAATTG
3001  TTGCCGGGAA  GCTAGAGTAA  GTAGTTCGCC  AGTTAATAGT  TTGCGCAACG  TTGTTGCCAT
3061  TGCTACAGGC  ATCGTGGTGT  CACGCTCGTC  GTTTGGTATG  GCTTCATTCA  GCTCCGGTTC
3121  CCAACGATCA  AGGCGAGTTA  CATGATCCCC  CATGTTGTGC  AAAAAAGCGG  TTAGCTCCTT
3181  CGGTCCTCCG  ATCGTTGTCA  GAAGTAAGTT  GGCCGCAGTG  TTATCACTCA  TGGTTATGGC
3241  AGCACTGCAT  AATTCTCTTA  CTGTCATGCC  ATCCGTAAGA  TGCTTTTCTG  TGACTGGTGA
3301  GTACTCAACC  AAGTCATTCT  GAGAATAGTG  TATGCGGCGA  CCGAGTTGCT  CTTGCCCGGC
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3361  GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA

3421  ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA

3481  ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG

3541  AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG

3601  AATACTCATA CTCTTCCTTT TTCAATCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC

3661  CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTCTG

3721  CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG

3781  GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATACCA

3841  AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG

3901  CCTACATACC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG

3961  TGTCTTACCG GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA

4021  ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC

4081  CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT

4141  CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC

4201  TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA

4261  TGCTCGTCAG GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC

4321  CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG

4381  GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG

4441  CGCAGCGAGT CAGTGAGCGA GGAAGCCGGC GATAATGGCC TGCTTCTCGC CGAAACGTTT
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4501    GGTGGCGGGA CCAGTGACGA AGGCTTGAGC GAGGGCGTGC AAGATTCCGA ATACCGCAAG

4561    CGACAGGCCG ATCATCGTCG CGCTCCAGCG AAAGCGGTCC TCGCCGAAAA TGACCCAGAG

4621    CGCTGCCGGC ACCTGTCCTA CGAGTTGCAT GATAAAGAAG ACAGTCATAA GTGCGGCGAC

4681    GACCGGTGAA TTGTGAGCGC TCACAATTCT CGTGACATCA TAACGTCCCG CGAAAT
```

Figure 52. HLA peptide motif search results

User Parameters and Scoring Information	
method selected to limit number of results	explicit number
number of results requested	20
HLA molecule type selected	A_0201
length selected for subsequences to be scored	9
echoing mode selected for input sequence	Y
echoing format	numbered lines
length of user's input peptide sequence	803
number of subsequence scores calculated	795
number of top-scoring subsequences reported back in scoring output table	20

Scoring Results			
Rank	Start Position	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1	425	MMPKYLNFV	1080.239
2	410	KLYVRRVFI	642.660
3	557	RLLKKGYEV	257.342
4	203	FLVADKVIV	131.175
5	144	LLHVTDTGV	118.238
6	547	KEAESSPFV	106.738
7	639	RLTESPCAL	87.586
8	381	VTFKSILFV	76.863
9	3	ALWVLGLCC	41.234
10	6	VLGLCCVLL	36.316
11	189	SELIGQFGV	29.023
12	741	RMLRLSLNI	27.879
13	451	LQQHKLLKV	27.573
14	280	YVWSSKTET	24.895
15	259	LELDTIKNL	24.638
16	417	FITDDFHDM	24.478
17	467	KTLDMIKKI	17.695
18	463	KLVRKTLDM	17.388

19	429	YLNFVKGVV	17.053
20	197	VGFYSAFLV	16.564

Figure 53. Suggested models for transmembrane topology for ICT1025

-----> STRONGLY prefered model: N-terminus inside
2 strong transmembrane helices, total score : 2962
from   to length score orientation
1   3   19 (17)   2034 i-o
2 191 212 (22)   928 o-i

------> alternative model
2 strong transmembrane helices, total score : 2607
from   to length score orientation
1   3   19 (17)   1929 o-i
2 191 213 (23)   678 i-o

Figure 54.."DAS" - Transmembrane Prediction server ICT 1025

Potential transmembrane segments

Start	Stop	Length	~	Cutoff
6	18	13	~	1.7*
7	17	11	~	2.2
195	209	15	~	1.7*
197	206	10	~	2.2
247	248	2	~	1.7
384	390	7	~	1.7
710	723	14	~	1.7
713	719	7	~	2.2*
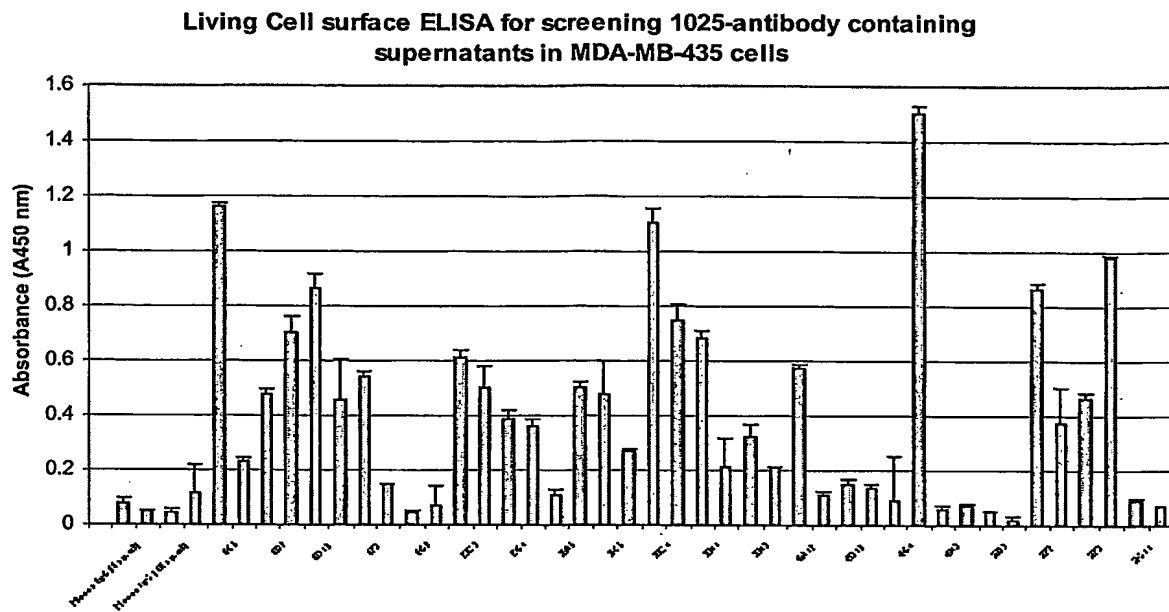
Figure 55. Screening of ICT1025 mAb for surface binding activities in breast tumor
cell
The culture supernatants from 40 ICT1025 mAb secreting hybridoma clones were
screened for the cell surface binding activities in MDA-MB-435 cells using a live cell
surface staining ELISA assay. Mouse IgG at various concentration were used as non-
specific controls. The clones with the highest cell surfsce binding activities
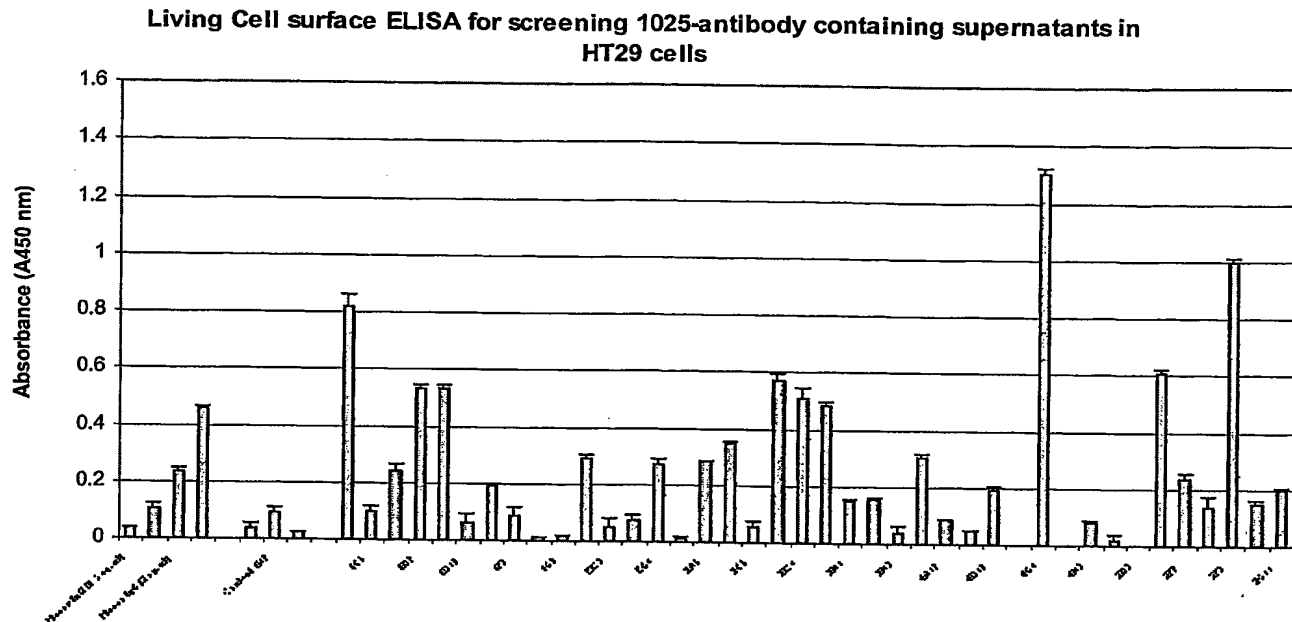(Absorbance value) were selected for mAb purification.

Figure 56. Screening of ICT1025 mAb for surface binding activities in colon tumor cells

The culture supernatants from 40 ICT1025 mAb secreting hybridoma clones were screened for the cell surface binding activities in HT29 cells using a live cell surface staining ELISA assay. Mouse IgG at various concentration were used as non-specific controls. Also, the supernatants from 3 GST mAb secreting hybridoma clones (2H2, 1H2, 3G3) were used as negative controls. The clones with the highest cell surfsce binding activities (Absorbance value) were selected for mAb purification.
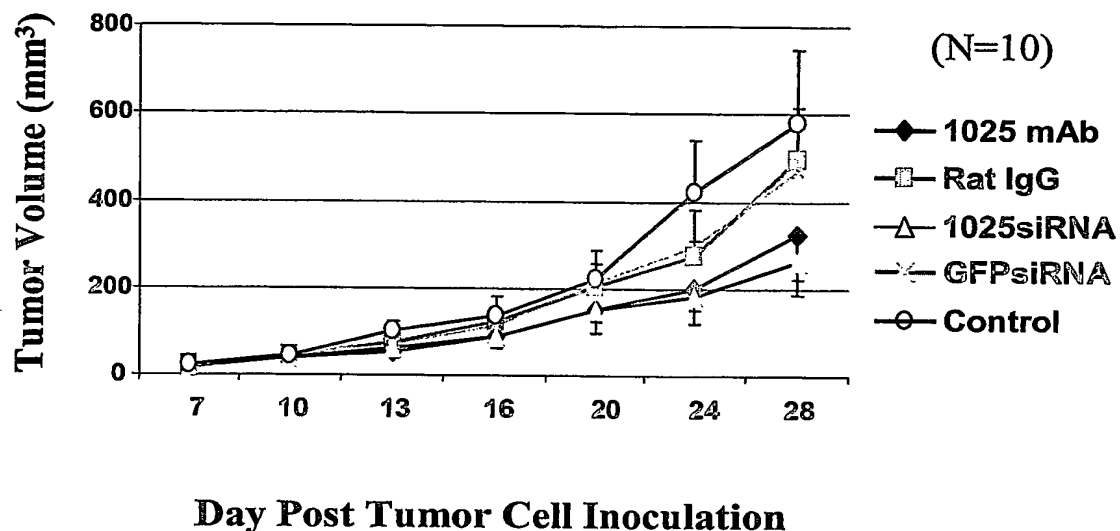
Day Post Tumor Cell Inoculation

Figure 57. Effect of inhibition of 1025 by antibody or siRNA on tumorigenesis and tumor growth. For antibody treatment, 5 million MDA-MB-435 cells were pre-incubated with 100 ug of 1025 mAb or Rat IgG in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site. For siRNA treatment, 5 million MDA-MB-435 cells in were transfected with 10 ug of 1025 siRNA or GFP siRNA using electroporation, then cells were incubated in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site. For control group, 5 million MDA-MB-435 cells were incubated in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site.